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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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sw model using - protein search, OM protein

1999, 00:50:47 9 November Run on:

/ ; Search time 13.18 Seconds
(without alignments)
609.225 Million cell updates/sec

US-09-072-994-14 1791 1 MKLSDYYIDKELIYNSAISD.....IRYDRSKRITSKEILQLMLD 339 score: Title: Perfect sc Sequence:

**BLOSUM62** Scoring table: 188963 segs, 23686106 residues Searched:

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		ALDICALIS CAN AC	Ar Ailase, scil DK2-groom fluo	reen fluorescen	omo sabiens Cdr	za sativa Cd	Oncoprotein	Smolality	Saccharomyc	activated	stress-acti	mitogen-ac	n MAP kinase	2-CD	ss activated	n CSBP beta	protein. New	dida albicans	ase #1. W	o sapiens Cdc2	us norvegicu	Oncoprotein	1-green floure	-green fl	icella nidula	CSBP2. New	ytokine suppress	uman monocy	38-green floures	-green floures	tress activated	tress activate	tress activated	ylic acid in	n MAP kinase	nding pr	n CSBP1. New	kine suppre	an monocyte	AP kinase	ccharomyces ce	jellomyces ca	man ERK-5. Ex
SUMMARIES	ΩI	1 2 2	- 1	8502	W85029	9568	9569	7076	9679	9268	40	2596	2378	2657	S D	8940	9407	155	268	1551	568 -	568	076	200	W85018	268 2	167	982	0,0	501	5	941	8941	8941	6125	900	6545	7167	4982	4906	1551	9568	9	6070
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ESULT 1  W99578 standard; P1 W99578; Z2-JUN-1999 (firs) C.albicans Cdk act; Protein kinase; cyc screening assay; for Candida albicans. W99907836-1999; I1-AUG-1999; F01788 I2-AUG-1999; FR-01( COMS) COMMISSARIA (COMS) COMISSARIA (COMS) COMMISSARIA (COMS) COMMISS	
W99578;  22-JUN-1999 (first 22-JUN-1999 (first C.albicans Cdk act: Protein kinase; cyc screening assay; fu Candida albicans. W09907836-Al.  18-FEB-1999. 11-AUG-1998; F01788 12-AUG-1997; FR-010 CCOMS) COMMISSARIA (COMS) COMISSARIA (COMS) COMMISSARIA (COMS) COMMISSARIA (COMS) COMISSARIA	A.A.
11-AUG-1998; F01788 12-AUG-1997; FR-01( COMS) COMMISSARIX (CURI-) INST CURIE (CURS) CNRS CENT PERYE G, Mann C, Thu WPI; 99-180489/15. N-PSDB; X27495. Candida albicans pr kinase activity antimycotic activity claim 3; Page 12-13 This sequence repre cyclin-dependent kinot cyclin dependent cyclin dependent cyclin-dependent cyclin-d	ase (CAK) in vivo (CIV) 1 protein. ent kinase activating kinase; Cdk; CAK
Candida albicans printings activity - antimycotic activity - Claim 3; Page 12-13 This sequence reprecyclin-dependent kinot cyclin dependent cy	TOMIQUE.
Claim 3; Page 12-13 This sequence reprecyclin-dependent kinot cyclin dependent kinot cides.  Query Match Best Local Similarity Augicides.  Sequence 339 AA;  Query Match INTESDYIDKELIY INTESPENDENT INTESPENDENT INTERFENDIKT INTERFENDI	penc
Query Match Best Local Similarity Matches 334; Conserv  1 MKLSDYYIDKELIY	French.  a protein kinase of the CIV1 family that has Cdk) -activating kinase (CAK) activity that is new member designated CAK in vivo (CIV1) f Saccharomyces cerevisiae, and lacks the mono acid. The sequence can be used screening y. against Candida albicans, or as industriations.
1 MKLSDYYIDKELIY 	core 1770; DB 1; Length 339; red. No. 6.8e-150; Mismatches 3; Indels 0; Gaps
61 PHPNITEYFNDLKI	AIDKFNNLPVCLKIVDEDFSLPPHSIHREIFILKTLK 60 
121 ANEIEEKDIKLWLK	YDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTL 120   :
181 LPPKDEPPMAKYID	QGIIHRDIKPSNIFFARDDITQPIIGDFDICYDLK 180 
241 DKELTNDSHVSDLY 	IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFOSVLVKD 240 
4	LLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDW 300 
QY 301 DIILPRCNDDLMKEIFTKMIRYDRSF 	SKRITSKEILQLMLD

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                     kinase;
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N-PSDB; V71073.

Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, particularly for identifying toxins and potential therapeutic agents
                                                                                                                                            study
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                     protein; MAP
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Human; CDK2 gene; fusion protein; green fluorescent protein; intracellular signalling; chimera.

Chimeric - Aequorea victoria.

Chimeric - Homo sapiens.
                                                                                                                                                                            or the invention. The gene
of a response mechanism for
cells causing cancers.
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                                                                                                                                                 This sequence is the MAP kinase of the invention contributes to the elucidation of a response mechenyironmental factors acting on call.
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Er A, Petersen Bjorn S.
n S;
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                       Mitogen activated protein;
                                              pombe.
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1996; JP-157503.
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15-OCT-1998.
07-APR-1998; DK0145.
07-APR-1997; DK-0003
                                  cancer.
Schizosaccharomyces I
J09313189-A.
09-DEC-1997.
29-MAY-1996; 157503.
29-MAY-1996; JP-15750
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WPI; 98-080080/08
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Example 12; Pages 208-209; 326pp; English.

The present sequence represents a human CDK2-green fluorescent protein C (GFP) fusion protein. The fusion protein is used in an assay to exemplify the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emission is processed to provide information that correlates spatial cemission to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, cespecially to screen for potential therapeutic agents or toxins, and to sequence 544 AA;
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Green fluorescent protein-CDK2 fusion product.

KW Human; CDK2 gene; fusion protein; green fluorescent protein; GFP;

KW intracellular signalling; chimera.

OS Chimeric - Aequorea victoria.

Chimeric - Homo sapiens.

PN W09845704-A2.

PD 15-OCT-1998.

PN W09845704-A2.

R Kasper A, Petersen Bjorn S, Scudder K. Thank

I Tullin S;

R WPI; 98-594401-77.
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Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, particularly for identifying toxins and potential therapeutic agent Example 12; Pages 212-213; 326pp; English.

The present sequence represents a green fluorescent protein (GFP)-1 CDK2 fusion protein. The fusion protein is used in an assay to exemplify the invention. The specification describes how quantitatin information about the influence of a molecule on a cellular responsinformation about the influence of
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26.28;
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WAYO-19980877/OT.

Gustafson MP, Leof EB, Limper AH, Thomas CF;

WPI: 99-080877/OT.

The dusqued or monitoring P. carinii

The sequence is that of a Cdc2 polypeptide.

The Cdc2 polypeptides are useful in treating P. carinii

The Sequence is that of a Cdc2 polypeptide.

The Cdc2 polypeptides are useful in treating P. carinii

C pneumonia in patients with chronic immunosuppression. Conditions

associated with P. carinii include acquired immune deficiency syndrome (AIDS), solid tumors, hematological malignancies, organ transplantation

and inflammatory conditions. The polypeptides are additionally useful

C AIDS), solid tumors, hematological malignancies, organ transplantation

and inflammatory conditions. The polypeptide and its antibodies are

and inflammatory conditions. The polypeptide and its antibodies are

c useful for diagnosing or monitoring P. carinii infection in patients.

The P. carinii Cdc2 polypeptides allow a therapeutic approach to treating

P. carinii pneumonia because they are not limited by significant side

effects. Polynucleotides encoding P. carinii Cdc2 enable in vitro
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obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in) directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and identify new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
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diagnosis; therapy;
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No. 2.4e-15;
~matches 119;
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Pred. No. 2.4e
59; Mismatches
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Homo sapiens Cdc2 protein kinase.
cdc2; protein kinase; diagnosis; infection;
AIDS; acquired immunodefiency syndrome; diagorgan transplantation.
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larity 26.2%;
Conservative
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                                                                         VYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL
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                                                                                                                                                           -AEMVTRRALFPGDSEIDQLF--
                                               56;
the
                                  298;
studying therapies.
                                               Indels
                                  Length
                                 Score 261; DB 1; ; Pred. No. 1.1e-15; 59; Mismatches 119;
developing new
                                                                                                : ]]
------TIGIPLPL
                                                                                                                                                      |:|||::|| | :||||| | LWYRAPEILLGSKYYSTAVDIWSLGCIF-
production of the protein, which (especially its life cycle) and (Sequence 298 AA;
                                                                                                                                                                                                                                                    AA
                                               59;
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                                 14.6%;
ilarity 26.2%;
Conservative 5
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RIFRTLGTPDEVVWPGVTSMPDY
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Matches 83
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WPI: 96-383673/38.

N-PSDB; 744328.

N-PSDB; 744328.

Yeasts contg, mutated HOG gene or multiple copies of HOG gene - have reduced or increased glycerol production

Example 5; Fig 5; 28pp; English.

Cow glycerol fermentation products can be produced using mutant strains of yeast, e.g. Saccharomyces sp. or Torulaspora sp., that have a reduced glycerol prodn. relative to the unmutated parental strain. High compositive fly glycerol prodn. relative to the unmutated parental strain. Hog2 and HOG4. Yeast strains contg. mutant HOG genes have a reduction in glycerol biosynthesis and are useful in prodn. of novel beverages, baked goods or glycerol. HOG1 and HOG2 are defined as yeast genomic DNA segments capable of complementing the reduced growth in high osmolarity media (defined as the OsmS phenotype) and glycerol biosynthesis defect of HOG1 and hog2 mutants, respectively. Southern blot hybridisation of HOG1 to chromosome XII. The present sequence is that of the HOG1 gene product of 416 amino acids with a mol. wt. of 47 kDa.
                                                                                248
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                                                                               KPHPNII ---EYFNDLKIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSN
  CYDLKLPPKDEPP
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 416;
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                                                                                                                                                                                                                                                                                                                                                                                    W06795 standard; Protein; 416 AA.
W06795;
27-JAN-1997 (first entry)
High Osmolality Glycerol 1 gene product.
HOG1; hog1; hog2; HOG2; mutant; glycerol; production; recentaromyces cerevisiae.
Saccharomyces cerevisiae.
US5545556-A.
13-AUG-1996.
23-MAY-1991; 704943.
18-MAR-1993; US-032382.
(UYRI-) UNIV RICE WILLIAM MARSH.
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les 103;
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23.1%;
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WPI; 96
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Homo sapiens.

Homo sapiens.

Homo sapiens.

MO9503323-A.

D2-FEB-1995.

18-JUL-1994; U08119.

R 19-JUL-1993; US-094533.

R 25-MAR-1994; US-220602.

(WFMA-) UNIV CALIFORNIA.

(UYMA-) UN
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-IKSYLYQILRGVAYCHSHRVLHRDLKPQNLLI--DRRTNALKLADFGLARAF
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GIPVRTFTH-----EVVTLWYRAPEILLGSRQYSTPVDMWSVGCIF-
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   1.7e-15;
thes 132;
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Pred. No. 5.3e-15;
9; Mismatches 112;
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R70768;
13-OCT-1995 (first entry)
JNK2 Oncoprotein polypeptide kinase; JNK; c-Jun;
Oncoprotein; polypeptide kinase; JNK; c-Jun;
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Pred. No. 1.,
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   larity 25.3%; P
Conservative 60;
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ilarity 27.1%;
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DD 209 LFPGDSEIDEIFKIFQVLGTPNEEVWPGVTLLQDYKSTFPRWKRMDLHK 258	KEIF -	258 VVPNGEEDAI-ELLSAMLVYDPAHRI	RESULT 10 R89409 ID R89409 standard; Protein; 423 AA.	89409; 5-APR-1996 (first entry) tress activated protein kinase tress activated protein kinase;	oflammation; hypoxia; hattus sp.	1995. 1995, 148898. 1994; US-240014. GEN HOSPITAL CO	ONTA-) ONTARIO CANCER wruch J, Banerjee P, PI; 96-106355/12.	-PSDB; T10639. NA encoding recombinant P54 str elated antibodies, useful for t eat stress, and for drug screen	laim 4; Page 35-36; 68pp; English. new family of proline-directed stress-activated pro SAPK), designated 054 alpha-I, alpha-II, beta-I, bet	amma (R89408-12, respectively), are products of a set of cDNA lones (see T10638-42) isolated from the brain cDNA library of cycloheximide-treated rat. The SAPK p54 proteins are strongl	ctivated by heat shock, tumour necrosis factor, interle phingomyelinase, chemical protein synthesis inhibitors schaemia. They have potential utility in the modulatio	nflammatory response and the up-regulation of rotective cellular proteins following injury equence 423 AA;	Query Match Best Local Similarity 27.1%; Pred. No. 6.4e-15; Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps	Qy 21 IYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREIFILKTLKPHPNIIEYFNDL 72 :     :   :	73 KIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANEIEEKDIKLW 13 : :       :  :       :  :  :     :  :  :	133 LKSMSSGLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPPKDEPP 18       :::	189 MAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELINDS 24      :   :   :   :   :     186VVTRYRAPEVILGM-GYKENVDIWSVGCIMGELVKGCVIFQGTD 22	249 HVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFN  :      :      :       230 HIDQWNKVIEQLGTPS-AEFMKKLQPTVRNYVEN	Qy 302 IILPRCNDDLMKEIFTKMIRYDRSKRITSKEILQ 335     : :::  :      :    :   Db 279 -IFPSESERDKIKTSQARDLLSKMLVIDPDKRISVDEALR 317	RESULT 11
QY 237 LVKDDKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYP 296	DD 210 MIEGKPLFPGKDHVHQFSIITDLLGSP	OY 297 RKDWDIILPRCNDDLMK	332 EIL 334 :	295 D SULT 9	5585 W95686	M25000; 08-JUN-1999 (firs Schizosaccharomyce cdc2; protein kina AIDS; acquired imm	organ transplantation. Schizosaccharomyces pombe. WO9856799-A1.	17-DEC-1998. 12-JUN-1998; U12100. 13-JUN-1997; US-874347. (MAYO-) MAYO FOUNDATION.	Gustafson MP, Leof EB, Limper AH, Thomas CF; WPI; 99-080877/07. New isolated polynucleotide encoding a Pheumocystis carini	polypeptide - useful for diagnosing or monitoring P. carinii infection in patients with chronic immunosuppression Example; Page 41; 67pp; English.	The sequence is that of a Cdc2 polypeptide. The Cdc2 polypeptides are useful in treating P. carinii pneumonia in patients with chronic immunosuppresion. Condition	associated with P. carinii include acquired immune del (AIDS), solid tumors, hematological malignancies, organd inflammatory conditions. The polypeptides are additional inflammatory conditions.	sectivitying agence that inhibit the phosphorylation activity.  carinii Cdc2 polypeptides. The polypeptide and its antibodi seful for diagnosing or monitoring P. carinii infection in polype P. carinii dection in polypeptides allow a therapeutic approach to carinii pheumonia because they are not limited by signification.	errects. Forynucleotides encoding F.carinii cdcz enable in production of the protein, which can be used in studying t (especially its life cycle) and developing new therapies. Sequence 297 AA;	Query Match Best Local Similarity 24.3%; Pred. No. 3.3e-15; Matches 81; Conservative 70; Mismatches 131; Indels 51; Gaps 11;	Qy 7 YIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREIFILKTLKPHP 63           :   :   :   :   :   :   :   :	Qy 64 NIIEYFNDLKIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANE 123       :::   : :    : :        63 NRSNCVRLLDILHAESKLYLVFEFLDMDLKKYMDRISETGATS 105	QY 124 IEEKDIKLWLKSMSSGLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPP 183 ::::::::::::::::::::::::::::::::::::	QY 184 KDEPPMAKYI-DVSTGIYKAPELILGITNYEYBIDIWSLGIILTGLYSENFQSVLVKDDK 242  :   ::    :   :   :	QY 243 ELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDWDI 302

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                  agents
Claim 1; Fig 1; 119pp; English.
The present claimed sequence represents the human stress-activated
protein kinase 4 (SAPK4) encoded by the SAPK4 cDNA which was isolated
from a human pituitary gland cDNA library. The invention claims that
from a human pituitary gland cDNA library. The invention claims that
SAPK4 protein can be useful in a screening assay for identifying agents
that inhibit its activity and/or agents that block its activation throug
stress activated kinase kinase 3 (SKK3). Therefore, the agents
identified in the assays may be potentially useful for treating
inflammatory diseases, e.g. rheumatoid arthritis, asthma and psoriasis.
Sequence 365 AA;
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Human mitogen-activated protein kinase homologue SMAP.
MAP kinase; gastritis; ulcer; viral infection; bacterial infection; neoplasm; stomach; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELPKTYVSPTHVGSGAYGSVCSAIDKRSGEKVAIKKLSRPFQSEIFAKRAYRELLLLKHM
                                                                                                                                                                                                                                                                                                                                                                                                                                      KLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDF -- SLPPHSIHREIFILKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NDKAAKSYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LTGLY
                                                                                                                                                                                                               screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DFGLARHADAEMTGY - - VVTRWYRAPEVILSWMHYNQTVDIWSVGCIMAEMLTG -
                                                                                                                                                                                                                           immuno-suppressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                          365;
                                                        y gland; as
arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DICYDLKLPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGII--
                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                              drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334
        W55967 standard; Protein; 365 AA.
W55967;
29-SEP-1998 (first entry)
Human stress-activated protein kinase 4 (SAPK4).
Stress-activated protein kinase 4; SAPK4; pituitary stress activated kinase kinase 3; SKK3; rheumatoid apportasis; inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LTQILKVTGVPG-TEFVQKL
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Pred. No. 8e-15;
57; Mismatches 125;
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and in
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Cohen P, Goedert M;
WPI; 98-240806/21.
N-PSDB; V26081.
New stress-activated protein kinase 4 - u
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98
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Best Local Similarity 26.1%;
Matches 90; Conservative
                                                                                                                                                                 COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                         Homo sapiens.
W09815618-A1.
16-APR-1998.
09-OCT-1997; G02779.
15-MAY-1997; GB-009781.
09-OCT-1996; GB-021096.
(MEDI-) MEDICAL RES COUNCOhen P, Goedert M;
WPI; 98-240806/21.
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Key
Misc_difference
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W23783;
29-OCT-1997
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SMAP
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                                                                                                                                                                                                                                                                                                                                                                       viral
                                                                                                                                                                                                                                                            The present sequence represents the novel human mitogen-activated protein (MAP) kinase homologue designated SMAP. The CDNA encoding was isolated from a human stomach cDNA library. The SMAP protein specifically involved with protective cell signalling processes at the products can be used in the study, diagnosis and treatment of conditions which affect the stomach such as gastritis, ulcers, vinand bacterial infections, or neoplasms associated with abnormal signally.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELPKTYVSPTHVGSGAYGSVCSAIDKRSGEKVAIKKLSRPFQSEIFAKRAYRELLLLKHM
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                                                                                                                                                                                                      e.g. gastriti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --MGMEFSEEKIQYLVVQMLKGLKYIHSAGVVHRDLKPGNL-AVNEDCELKIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                    used to
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ulcer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
                                                                                                                                                                                 DNA encoding human mitogen-activated protein kinase develop prods. for the diagnosis and treatment of, ulcers, viral and bacterial infections or neoplasms Claim 1; Page 28-29; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LTQILKVTGVPG-TEFVQKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 251.5; DB 1;
Pred. No. 9.8e-15;
5; Mismatches 125;
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mitogen-activated Fammation; gastritis; t
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 "Gly encoded by
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Human MAP kinase homologue SMAP.
SMAP; MAP kinase homologue; mítogen
signal transduction; inflammation;
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 14.0%;
Similarity 26.4%;
91; Conservative
                WO9702347-A1.
23-JAN-1997.
28-JUN-1996; U11170.
30-JUN-1995; US-000722.
(INCY-) INCYTE PHARM INC.
Au-Young J, Guegler KJ, H
WPI; 97-108960/10.
N-PSDB; T78543.
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02-SEP-1997.
28-JUN-1996; 674612.
28-JUN-1996; US-674612.
(INCY-) INCYTE PHARM INC.
Au-Young J, Guegler KJ, E
WPI; 97-447978/41.
N-PSDB; T90352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
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/note=
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W26578;
20-JAN-1998
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Best Local
Matches 8
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R89408;
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                                                                             This polypeptide sequence comprises SMAP, a human MAP kinase homologue that is involved in protective cell signalling processes. Its amino acid sequence was deduced from a claimed isolated polynucleotide (see T90352) obtained from a stomach cDNA library. Also claimed are: an expression vector containing the polynucleotide can be used in drug screening, drug design, research, antibody production, and in methods for the diagnosis and treatment of activated or inflammed cells and/or tissues associated with the expression of SMAP, especially for the diagnosis and treatment of conditions that affect the stomach such as gastritis, ulcers, viral and bacterial infections and neoplasms.
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ur; agonist;
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P. CDK4 binding proteins ing test compounds as
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                                   homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                              73;
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-5-CDK-BP clone #227 derived CDK4 binding protein.
cycle; CDK4; regulation; G1 phase; proliferation; twin dependent kinase; differentiation; CDK4 inhibitor;
                                                                                                                                                                                                                                                                                     Length
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                                             of
                                 protein kinase
for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
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N-PSDB; T12180.
Cyclin-dependent kinase-4 binding protein - used in t (ant)agonists of cell cycle regulation.
Claim 1; Page 87-88; 115pp; English.
R90533-R90556 are cyclin dependent kinase 4 (CDK4) bi encoded by clones of the plasmid pJG4-5-CDKBP. CDK4 kencoded by clones of the plasmid pJG4-5-CDKBP. The complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LIQILKVIGVPG-TEFVQKL
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125;
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                                                                                                                                                                                                                                                                                   Score 251.5; D
Pred. No. 9.8e-
                                                                                                                                                                                                                                                                                                  d. No. 9.86
Mismatches
for production of recombinant protein, finflammation Claim 1; Column 21; 19--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                                                                                                                                                                                                                                  th 14.0%;
Similarity 26.4%;
91; Conservative
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Synthetic.
W09533819-A2.
14-DEC-1995.
02-JUN-1995; UG7113.
02-JUN-1994; US-253155.
"MITO-) MITOTIX INC.
Gyuris J;
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96-040227/04.
DB; T12180.
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y implicated in the control of the early are strong candidates for controlling is and the onset of cancer. Nucleic acids of these may be used as probes/primers
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Claim 2; Page 34-35; 68pp; English.

A new family of proline-directed stress-activated protein kinases

C SAPK), designated p54 alpha-I, alpha-II, beta-I, beta-II and gamma (R89408-12, respectively), are products of a set of cDNA clones (see T10638-42) isolated from the brain cDNA library of a cycloheximide-treated rat. The SAPK p54 proteins are strongly activated by heat shock, tumour necrosis factor, interleukin-I-beta, sphingomyelinase, chemical protein synthesis inhibitors and ischaemia. They have potential utility in the modulation of the inflammatory response and the up-regulation of repair or protective cellular proteins following injury or chemical insult.
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and D-type cyclins are strongly implicated in the control of the G1 phase of the cell cycle and are strong candidates for control and/or preventing tumourigenesis and the onset of cancer. Nucleic encoding CDK4-BP or fragments of these may be used as probes/print to diagnose the presence or absence of genetic lesions in a gene encoding 1 of the 24 CDK4-BP, and hence to diagnose the risk for subject of developing a cell-proliferation associated disorder (examples of the control of th
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Stress activated protein kinase p54 alpha-I.
Stress activated protein kinase, SAPK; p54 all
inflammation; hypoxia; heat stress.
Rattus sp.
CA2148898-A.
10-NOV-1995.
08-MAY-1995, 148898.
09-MAY-1995; 148898.
(GEHO ) GEN HOSPITAL CORP.
(GHO ) GEN HOSPITAL CORP.
(ONTA-) ONTARIO CANCER INST.
Avruch J, Banerjee P, Kyriakis JM, Woodgeti WPI; 96-106355/12.
N-PSDB; T10638.
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Search completed: November 6, 1999, 07:28:06 Job time: 23839 sec

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 version -
GenCore
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sw model nsing - protein search, OM protein

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; Search time 16.13 Seconds
(without alignments)
1293.447 Million cell updates/sec

US-09-072-994-14 1791 1 MKLSDYYIDKELIYNSAISD.. Title: Perfect score: Sequence:

339 ....IRYDRSKRITSKEILQLMLD

**BLOSUM62** Scoring table: 61543640 residues seds, 201082 Searched:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

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5 63 880 19 70 70	DB 5; Length 311; 9e-11; s 117; Indels 85; Gaps
21 63 80 19 70 70	DEDFSLPPHSIHREIFILKTLKPH 62
63 PNIIEYF       :   80 PNIVNLL   19 TLANEIE   20   79 LKLPPKD   : :   70 FQV	:   :   :    DRTEEGIPQTALREVSILQEF-DH 79
80 PNIVNLL 19 TLANEIE 20 79 LKLPPKD ::	-NDLKIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQY 118
19 TLANEIE 20 79 LKLPPKD :: 70 FQV	:   :  KQEGGYSG 120
2079 LKLPPKD :: 70 FQV	PSNIFFARDDITQPIIGDFDICYD 178
79 LKLPPKDEPPMAKYI :: 10 FQVPMHTYT	:   PANILLTSGNVLKLADFGLARA 169
70 FQVPMHTYT	YEIDIWSLGIILTGLYSENFOSVL 237
	:     :   ::   :  :  :     HEVVTLWYRAPEILLGEKHYAPAVDMWSVGCIFAELARRKVL 220
238 VKDDKELTNDSHVSDLYLLNQIFENFGTP	LYLLNQIFENFGTPNLTDFEDELFCDEYNNENLH 286
221 FRGDSEIGQLFEIFQVLGTPTDTEG	:  :     LFEIFQVLGTPTDTEGSWPGVSRLPDYRDV 260
287 FKKFNLQKYPRKDWDIILPRCNDDLMKEIFTKMIRYDRSKRITSKEILQ	ORSKRITSKEILQ 335
:   : : : :   : : :     260FPKWTAKRLGQVLPELHPDAI-DLLSKMLKYDPRERISAKEALO	:  ::      OPRERISAKEALO 302

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                                                                                                Leishmania
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                                                                                                                                                                                                                                                                           DRYNRLDVLGEGTYGVVYRAVDKITGQYVALKKVRLDRTEEGIPQTALREVSILQEF
                                                                                                                               WANG Y., DIMITROV K., GARRITY L.K., SAZER S., BEVERLEY S.M.; "Stage-specific activity of Leishmania major CRK3 kinase and functional rescue of a Schizosaccharomyces pombe cdc2 mutant. Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF073381; AAD08994.1; -. PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                               Trypanosomatidae;
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---LFEIFQVLGTPTDTEGSWPGVSRLPDYRDV-
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                                                                                                                                                                                                                      Score 271.5; DB 5;
Pred. No. 1.9e-11;
3; Mismatches 117;
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                                                                                                                                                                                              CRC32;
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                                         Created)
Last sequence up
Last annotation
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                                                                                               Kinetoplastida;
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SEQUENCE FROM N.A.
STRAIN=LINE H;
MEDLINE; 96065755.
VINKENOOG R., VELDHUISEN B.,
JANSE C.J., WATERS A.P.;
"Comparison of introns in a contraction species.";
Mol. Biochem. Parasitol. 71:27
                                                                                                                                                                                              35644 MW;
                                          10,
10,
                                                                                                                                                                                                                      th 15.2%; Similarity 26.9%; 94; Conservative
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                                          (TrEMBLrel.
(TrEMBLrel.)
(TrEMBLrel.)
                                                                                     Leishmania major.
Eukaryota; Euglenozoa;
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01-MAY-1999 (TrEMBLrel
01-MAY-1999 (TrEMBLrel
CDC2-RELATED KINASE 2.
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Alveolata;
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                                                                                                                                                                                              311 AA;
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01-MAY-1999 (7
CDC2-RELATED R
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096821;
01-MAY-1999
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Eukaryota;
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                                                                                               Eukaryota;
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WATANABE Y.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB012146; BAA25200.1; -.
PFAM; PF00069; pkinase; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SEQUENCE 407 AA; 46428 MW; 56BDD207 CRC32;
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103;
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[2]
SEQUENCE FROM N.A.
STRAIN=LINE H;
VINKENOOG R., SPERANCA M.A., RAMESAR J., THOMAS
DEL PORTILLO H.A., JANSE C.J., WATERS A.P.;
"Characterisation of the Cdc2-related kinase 2
knowlesi and P. berghei.";
Mol. Biochem. Parasitol. 95:229-240(1998).
EMBL; AJ224155; CAA11852.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHOG1.
Zygosaccharomyces rouxii (Candida mogii).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Zygosaccharomyces.
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Similarity 27.5%;
84; Conservative
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LLEZ-INON M.T.;
otein kinase from Trypanosoma cruzi that
ins.";
37-351(1998).
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---LIDFEDELFCDEYNNENLHFKKFN 291
                           ---KSA 240
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EGIPQTALREVSILQEIH-HPNVVNLLDVICTDGKL 95
                                                                                                                                                                                                                                                   plastida; Trypanosomatidae; Trypanosoma
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-KRGCTFT-GVT------LKKLVY
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Pred. No. 6.5e-11;
Mismatches 99;
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OPAERISAKEALQ 302
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8540A103 CRC32;
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SEQUENCE FROM N.A.
STRAIN=ANKARA;
MEDLINE; 97084571.
KINNAIRD J.H., LOGAN M., KIRVAR E., TAIT A., CARRINGTON M.;
KINNAIRD J.H., LOGAN M., KIRVAR E., TAIT A., CARRINGTON M.;
The isolation and characterization of genomic and cDNA clones coding for a cdc2-related kinase (ThCRK2) from the bovine protozoan parasite Theileria.";
Mol. Microbiol. 22:293-302(1996).
EMBL; X98768; CAA67306.1; -.
PFAM; PF00069; pkinase; 1.
SEQUENCE 298 AA; 34230 MW; BF4362AE CRC32;
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64
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| : |:: :| |||: |:| || ||
182 YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMIFRKEPF------
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                                     DYOLVRKL-GRGKYSEVFEAINITNNEKVVVKILK---PVKKKKIKREIKILENLRGGPN
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Pred. No. 9.1e-11
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larity 24.9%;
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Best Local Similarity
Matches 85; Conser
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Q26671;
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Q1-NOV-1996
Q1-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
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T.H., JUST D., ROTHAN
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RELATED SEQUENCE 4
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1.1e-10;
ches 125;
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                                                                                            SEQUENCE FROM N.A.
STRAIN=CV. WEST VIRGINIA 106; TISSUE=FRUIT;
JOUBES J., CHEVALIER C., PHAN T.H., JUST D., ROT
BERGOUNIOUX C., RAYMOND P.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ da
EMBL; Y17225; CAA76700.1; -.
PFAM; PF00069; pkinase; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SEQUENCE 294 AA; 33751 MW; 75F8C00C CRC32;
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STRAIN=B10.A/AKR;
CHEN L., HARDWICK J.P., SITKOVSKY M.V.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ
EMBL; U51866; AAA96795.1; -.
MGD; MGI:894650; CSNK2A1-RS4.
PFAM; PF00069; pkinase; 1.
SEQUENCE 391 AA; 45179 MW; 888B30D7 CRC32;
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Q1-NOV-1998 (TrEMBLrel. O
Q1-NOV-1998 (TrEMBLrel. O
CASEIN KINASE II, ALPHA 1
(CASEIN KINASE II, ALPHA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
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P79996;
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
C-JUN AMINO-TERMINAL KINASE-2 ALPHA1.
JNK2-ALPHA1.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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STRAIN=51-S;
MEDLINE; 95210349.
TANG L., PELECH S.L., BERGER J.D.;
"Isolation of the cell cycle contratraurelia.";
Biochim. Biophys. Acta 1265:161-16
EMBL; U15802; AAA79977.1; -.
PFAM; PF00069; pkinase; 1.
SEQUENCE 307 AA; 35305 MW; EIC
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Pred. No. 1.7e-10;
58; Mismatches 126;
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Pred. No. 1.6e-10;
); Mismatches 109
                                            TANDA
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SEQUENCE FROM N.A.
TISSUE=BRAIN;
MEDLINE; 97320448.
ISHIKAWA T., NAKADA-MORIYA Y., AN
MINATOGAWA Y., NOHNO T.;
"Expression of the JNK2-alphal ge
Biochem. Biophys. Res. Commun. 2;
EMBL; AB000807; BAA19188.1; -.
PFAM; PF00069; pkinase; 1.
SEQUENCE 382 AA; 44009 MW; 39
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MEDLINE; 93131026.
DEVILAT I., CARVALLO P.;
"Structure and sequence of an i iI-alpha subunit.",
FEBS Lett. 316:114-118(1993).
EMBL; X70251; CAA49758.1; -.
PFAM; PF00069; pkinase; 1.
SEQUENCE 391 AA; 45156 MW;
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| YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMIFRKEPF------
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O62618;
O62618;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1999 (TrEMBLrel. 10, Last sequence update)
O1-AUG-1999 (TrEMBLrel. 10, Last annotation update)
P38A MAP KINASE.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.
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Mol. Cell. Biol. 18:3527-3539(1998).
EMBL; AF035547; AAC39031.1; -.
EMBL; AF035546; AAC39030.1; -.
FLYBASE; FBgn0015765; Mpk2.
PFAM; PF00069; pkinase; 1.
SEQUENCE 366 AA; 42255 MW; F6E3EEED CRC32:
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Pred. No. 1.7e-10;
1; Mismatches 130;
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Similarity 25.08;
86; Conservative (
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040482;
040482;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 01, Last sequence
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                                                                                                                                                                                                                                                PRELIMINARY; PRT; 380 AA.

093982

093982;

01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

01-MAY-1999 (TrEMBLrel. 10, Last annotation update)

PUTATIVE MAP KINASE.

HOG1.

Zygosaccharomyces rouxii (Candida mogii).

Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomyces saccharomycetaceae; Zygosaccharomycesc.

[1]

SEQUENCE FROM N.A.

STRAIN=CBS 732;

KINCLOVA O., SYCHROVA H.;

KINCLOVA O., SYCHROVA H.;
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                                    307
: : : | | : : | | SLPPMKGRSFKNVFKNAN-PLAIDLLEKMLELDAEKRITAEEAL
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23.48;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIEEKD---IKLWLKSMSSGLEFIHSQGIIHRDIKPSNIFFARDDITQPI-IGDFDICY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
           Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 294
core eudicots; Asteridae; euasterids I; Solanales; Solanace
Nicotiana.
[1]
SEQUENCE FROM N.A.
STRAIN=XANTHI;
OIN L.X., PERENNES C., BERGOUNIOUX C.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77082; AAB02567.1; -.
MENDEL; 13986; NICta;2321;mn13986.
PFAM; PF00069; pkinase; 1.
PFAM; PF00069; pkinase; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SEQUENCE 294 AA; 33874 MW; 9B0479D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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14.4%; Score 257.5; DB 10;
Best Local Similarity 25.9%; Pred. No. 1.6e-10;
Matches 90; Conservative 54; Mismatches 122;
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6, 1999, 08:26:48 Search completed: November Job time: 771 sec

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## version 4.5 - 1998 Compugen Ltd. GenCore Copyright (c) 1993

using sw model - protein search, OM protein 1999, 14:48:40 5, November Run on:

; Search time 11.2 Seconds (without alignments) 855.621 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-072-994-14 1791 1 MKLSDYYIDKELIYNSAISD.....IRYDRSKRITSKEILQLMLD 339

**BLOSUM62** Scoring table: 77977 seqs, 28268293 residues Searched:

SwissProt\_37:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		QUYSYL SCRIZOSACCH D34112 diatwosteli	43568 saccharomy	48963 mesocr	23437 xenopus la	23111 zea mays	24941 homo sapie	21868 gallus gal	19138 homo sapie	19139 rattus no	43450 carassius	36615 schizosacc	54666 trypa	50737 mus muscul	28020	29618 oryza sati	12525 dictyo	33674 oryctolag	<b>00526 homo sap</b>	04551 schizosacc	32485 saccharomy	598	28547 theileria	7785 plasmodium	51958 carassius	19186 rattus nor	21869 gallus ga	24033 xenopus la	1042/ bos tauru	32207 candida	10231 schizosac	9/84 homo sapi	39620 oryza sat	3063 candid	  -  -	5567 xenopus l	)8466 arab	2720 dictyos	4923 medi	4100 arabid	7176 medicago s	2389 vigna unqu	0336 cyprinus c
SUMMARIES	H	Oddo tana	C2 DICDI	K1 YE	DK2_MESA	K2_XE	2_MA	$\kappa_2^{\kappa}$		$21_{-}$	C21_RAT	DK2_	SK1	23_TRYB	$\frac{1}{2}$	$\alpha'$	-,'		_   []	- 1	Υ'n.	ړ',	JNKZ_HUMAN	: اي	<u>. ای</u>	ی ا	KZ_KAT	7 C	۷'c	או או	HOGI_CANAL	4 C	NC22_HUMAN	0.170_/47	ς Σα Σα	χ   χ γ α	7. 7. 7.	C22_ 	ZA_D	21_MEDS	_ARAT	K1_MED	C2_VIGU	ထ
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Gaps

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Indels

Length 349;

Query Match
Best Local Similarity 26.9%; Pred. No. 2.7e-10;
Matches 93; Conservative 60; Mismatches 114;

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NP_BIND
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IT (BY
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                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA from Dictyostelium
                                                                                                                                                       -AEM
                                                                                                                                  DLKLPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVL
                                                                                                                                                                                                                                                                                                                                                          (P34 PROTEIN
                                                                                       YTLANEIEEKDIKLWLKSMSSGLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDICY
                                                                                                                                                                              -NNENLHFK
                      EITTRYSDLOPIGMGAFGLVCSAKDQLTGMNVAVKKIMKPFSTPVLAKRTYRELKLLKHL
                                            --YDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNO
 -PHSIHREIFILKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL CYCLE. IT IS REQUIRED IN HIGHER CELLS FOR ENTRY INTO SAND MITOSIS. P34 IS A COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA
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ACTIVATES
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THE CONSERVED CATALYTIC DOMAINS OF BELONGS TO THE CDC2/CDKX SUBFAMILY

BELONGS TO THE CDC2/CDKX SUBFAMILY
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                                                                                                                                               -TSR
                                                                                                             -PLETQFIQYFLYQILRGLKFVHSAGVIHRDLKPSNILINEN-
                                                                                                                                                                                                                                             -DLLEKMLVFDPRKRISAADAL
                                                                                                                                                                                                                         KFNLQKYPRKDWD11LPRCNDDLMKEIFTKMIRYDRSKRITSKEIL
  KLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLP-
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THR-162
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ON UPDATE)
OLOG (EC 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: PHOSPHORYLATION AT THE ENZYME, WHILE PHOSPHORYLATION AT THR-SIMILARITY).
SIMILARITY).
SUBUNIT: FORMS A STABLE BUT NON-COVALENT SUBUNIT AND WITH A CYCLIN.
SIMILARITY: WITH THE CONSERVED CATALYTIC SIMILARITY: WITH THE CONSERVED CATALYTIC PROTEIN KINASES. BELONGS TO THE CDC2/CDKX
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HSSP; P24941; 1AQ1
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10 288 PROTEIN KINASE.
16 24 ATP (BY SIMILARITY).
39 39 ATP (BY SIMILARITY).
129 129 BY SIMILARITY).
20 20 PHOSPHORYLATION (BY SI
21 21 PHOSPHORYLATION (BY SI
162 162 PHOSPHORYLATION (BY SI
296 AA; 33773 MW; 6AABD40A CRC32;
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Pred. No. 3.6e-10;
; Mismatches 122
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES
SACCHAROMYCETACEAE; SACCHAROMYCES.
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SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE; 95400292.
MURAKAMI Y., NAITOU M., HAGIWARA H., SHI
SASANUMA S.-I., SASANUMA M., TSUCHIYA Y.
YAMAZAKI M., TASHIRO H., EKI T.;
"Analysis of the nucleotide sequence of Saccharomyces cerevisiae.";
NAT. GENET. 10:261-268(1995).
-!- SIMILARITY: BELONGS TO THE CDC2/CDC2
PROTEIN KINASES.
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SEQUENCE FROM N.A.
MEDLINE; 96361353.
KALDIS P., SUTTON A., SOLOMON M.J.;
"The Cdk-activating kinase (CAK) fr
CELL 86:553-564(1996).
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 This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerenties requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-).
CDK2.
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.
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SEQUENCE FROM N.A.
MEDLINE; 94107363.
NOGUCHI E., SEKIGUCHI T., YAMASHITA K., NISHIMOTO
NOGUCHI E., SEKIGUCHI T., YAMASHITA K., NISHIMOTO
"Molecular cloning and identification of two types
"Molecular cloning and identification of two types
                                                                                                                                                  1.
FALSE_NEG.
                                                                                                                                                                                                                                                                       Score 267; DB 1;
Pred. No. 1.1e-09;
6; Mismatches 144
                                                                                                                                                                                              7THREONINE-PROTEIN KINASE;
368 PROTEIN KINASE.
156 BY SIMILARITY.
42186 MW; 743F447B CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                              EMBL; U60192; G1480664; -.
EMBL; D50617; D1009850; -.
SGD; L0003177; CAK1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS4941; 1AQ1.
TRANSFERASE; SERINE/THREONINE-PROTEIN KI
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Similarity 25.1%;
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368 AA;
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CAK) (BY SIMILARITY)
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PFAM; PF00069; pkinase; 1.

HSSP; P24941; 1AQ1.

TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING; CELL CYCLE; CELL DIVISION; MITOSIS; PHOSPHORYLATION.

OMAIN 4 286 ATP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).

MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).

MOD_RES 160 PHOSPHORYLATION (BY SIMILARITY).

MOD_RES 160 160 PHOSPHORYLATION (BY SIMILARITY).

SEQUENCE 298 AA; 33839 MW; 48FFB9B9 CRC32;
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ACTIVITY OF
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THR-160
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Pred. No. 9.5e-10;
9; Mismatches 118;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
KINASE 2 (EC 2.7.1.-) (
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- FUNCTION: PROBABLY INVOLVED IN THE COUNTING S PHASE AND G2.
- ENZYME REGULATION: PHOSPHORYLATION AT THE ENZYME, WHILE PHOSPHORYLATION AT SIMILARITY).
- SIMILARITY: WITH THE CONSERVED CATALY PROTEIN KINASES. BELONGS TO THE CDC2,
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4; Conservative
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CDK2_XENLA STANDARD

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01-NOV-1991 (REL. 20, C

01-NOV-1995 (REL. 32, L

01-OCT-1996 (REL. 34, L

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                                                            ANURA;
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SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. BELONGS TO THE CDC2/CDKX SUBFAMILY.
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                                                                                                                                                                                                             <u>[4</u>
                            XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION AT THR-160.

MEDLINE; 93345457.

POON R.Y.C., YAMASHITA K., ADAMCZEWSKI J.P., HUNT T., SHUTTLEW POON R.Y.C., YAMASHITA K., ADAMCZEWSKI J.P., HUNT T., SHUTTLEW "The cdc2-related protein p40M015 is the catalytic subunit of protein kinase that can activate p33cdk2 and p34cdc2.";

EMBO J. 12:3123-3132(1993).

-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYC INTERACTS WITH CYCLINS A, D, OR E.

-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INF THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT SIMILARITY).
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SIMILARITY).
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or send an em.

or send an em.

emal, x14227; G64666; -.

EMBL, x37871; A37871.

R PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PRAM; PF00069; pkinase; 1.

R HSSP; P24941; 1HCK.

KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDI
KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDI
FT NP_BIND 4 286 PROTEIN KINASE.

FT NP_BIND 10 18 ATP (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 160 PHOSPHORYLATION (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 160 PHOSPHORYLATION (BY CAK).

THE ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 160 PHOSPHORYLATION (BY SIMILARITY).

FT ACT_SITE 127 127 BY SIMILARITY.

FT MOD_RES 15 FROM BY SIMILARITY.

FT NAME BY SIMILA
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                                                                                                                                                                                                                    К.,
                                                                                                                                                                                                                                                                       CDNA
                                                                                                                                     SEQUENCE FROM N.A.

TISSUE=OVARY;

MEDLINE; 91126051.

PARIS J., LE GUELLEC R., COUTURIER A., LE GUELLEC
CAMONIS J., MACNEILL S., PHILIPPE M.;

"Cloning by differential screening of a Xenopus CI
protein highly homologous to cdc2.";

PROC. NATL. ACAD. SCI. U.S.A. 88:1039-1043(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 265; DB 1; Pred. No. 1.1e-09; Pred. No. 1.1e-10; Pred. No. 1.1e-10;
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SIMILARITY).
CAK) (BY SIMILARITY)
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COLASANTI J., TYERS M., SUNDARESAN V.;

COLASANTI J., TYERS M., SUNDARESAN V.;

"Isolation and characterization of cDNA clones encoding a functiona p34cdc2 homologue from Zea mays.";

PROC. NATL. ACAD. SCI. U.S.A. 88:3377-3381(1991).

-!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.

-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY SIMILARITY).

-!- SIMILARITY).

-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. BELONGS TO THE CDC2/CDKX SUBFAMILY.
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
POACEAE; ZEA.
                                                                                                                                             IFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDWDIILPRCNDDLMKEIFTK
                                                                                                                                                                                        -KSTFPKWIRQDFSKVVPPLDED-GRDLLAQ
IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDSHVSDLYLLNQ
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-ALFPGDSEIDQLF
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41; 1HCK.

E; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;

CELL DIVISION; MITOSIS; PHOSPHORYLATION.

4 287

PROTEIN KINASE.

4 287

ATP (BY SIMILARITY).

33 33 ATP (BY SIMILARITY).

127 127

BY SIMILARITY.

14 14 PHOSPHORYLATION (BY SIMILARITY)

15 15 PHOSPHORYLATION (BY SIMILARITY)

161 161 PHOSPHORYLATION (BY SIMILARITY)

161 PHOSPHORYLATION (BY SIMILARITY)
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L.5e-09;
les 123;
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Pred. No. 1.5e;
Mismatches
                                                    |:|||::|| | :||||| | :||||||| | : : wyrapeillgckfystavdiwslgcifaemitrr-
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MAIZEDB; 60686; -.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS00108; PROTEIN_KINASE_ST; 1

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

PFAM; PF00069; pkinase; 1.

HSSP; P24941; 1HCK.
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MEDLINE; 91195354
COLASANTI J., TYE
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TRANSFERASE;
CELL CYCLE; C
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120
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  -IVDEDFSLPPHSIHREIFILKTLKP
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MEDLINE; 92020980.
NINOMIYA-TSUJI J., NOMOTO S., YASUDA H., REED S.I., MATSUMOTO "Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a budding yeast cdc28 mutation.";
PROC. NATL. ACAD. SCI. U.S.A. 88:9006-9010(1991).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUKARYOTA; MAMMALIA; HOMINIDAE; HOMO.

[1]

SEQUENCE FROM N.A.

MEDLINE; 91330891.

ELLEDGE S.J., SPOTTSWOOD M.R.;

"A new human p34 protein kinase, CDK2, identified by of a cdc28 mutation in Saccharomyces cerevisiae, is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
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                                                                                                                                         HGNIVRLHDVVHSEKRIYLVFEYLDLDLKKFMDSCPEFAKNPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDK2_HUMAN STANDARD; PRT; 298 AA. P24941; 01-MAR-1992 (REL. 21, CREATED) 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JONES
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n of CDK2 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSAI L.-H., HARLOW E., MEYERSON M.;
"Isolation of the human cdk2 gene that
adenovirus ElA-associated p33 kinase.";
NATURE 353:174-177(1991).
[3]
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EDLINE; 93288132.
E BONDT H.L., ROSENBLATT J., JANCARIK
ORGAN D.O., KIM S.-H.;
Crystal structure of cyclin-dependent
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PHOSPHORYLATION SITES.
MEDLINE: 93010995.
GU Y., ROSENBLATT J., O'MORG
"Cell cycle regulation of CE
and Tyr15.";
EMBO J. 11:3995-4005(1992).
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EMBO J. 10:2653-2659(1991)
[2]
SEQUENCE FROM N.A.
MEDLINE; 91367262.
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MEDLINE; 97075215.
SCHULZE-GAHMEN U., DE BONDT H.L., KIM S.-H.;
"High-resolution crystal structures of human cyclin-dependent kinase 2 with and without ATP: bound waters and natural ligand as guides for inhibitor design.";
J. MED. CHEM. 39:4540-4546(1996).
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MEDLINE; 96182647.

BOURNE Y., WATSON M.H., HICKEY M.J., HOLMES W., ROCQUE W., REED S.I..

TAINER J.A.;

TAINER J.A.;

"Crystal structure and mutational analysis of the human CDK2 kinase complex with cell cycle-regulatory protein CksHs1.";

CELL 84:863-874(1996).

-!- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.

INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL DURING S PHASE AND G2.

-!- ENZYME REGULATION: PHOSPHORYLATION AT THR-160 ACTIVATES IT.

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THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT.

PROTEIN KINASES. BELONGS TO THE CDC2/CDKX SUBFAMILY.
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A
MEDLINE; 96313126.
RUSSO A.A., JEFFREY P.D., PAVLETICH N.P.;
"Structural basis of cyclin-dependent kinase activation by phosphorylation.";
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                                                                 POLYAK K., GIBBS E., HURWITZ
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e kinase.";
5-2740(1996).
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MEDLINE; 96181476.
DE AZEVEDO W.F. JR., MULEER-DIECKMANN H.-J., SC WORLAND P.J., SAUSVILLE E., KIM S.-H.;
"Structural basis for specificity and potency c "Structural basis for specificity and potency c inhibitor of human CDK2, a cell cycle kinase.";
                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMEMEDLINE; 95356811.
JEFFREY P.D., RUSSO A.A., POLYAK K., GIBBS E. MASSAGUE J., PAVLETICH N.P.;
"Mechanism of CDK activation revealed by the cyclina-CDK2 complex.";
NATURE 376:313-320(1995).
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MEDLINE; 97475219.
LAWRIE A.M., NOBLE M.E.M., TUNNAH P.,
ENDICOTT J.A.;
"Protein kinase inhibition by staurosp
the molecular interaction with CDK2.";
NAT. STRUCT. BIOL. 4:796-801(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorylation.";
NAT. STRUCT. BIOL. 3:696-700(1996)
NATURE 363:595-602(1993)
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P21868;
01-MAY-1991 (REL. 18, CREATED)
01-MAY-1992 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE: PHASTANTNAF. CAPT
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PIR; A38611; A38611.

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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PRAM; PF00069; pkinase; 1.
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MEDLINE; 91115855.

MARIDOR G., PARK W., KREK W., NIGG E.A.;

"Casein kinase II. cDNA sequences, developmental extissue distribution of mRNAs for alpha, alpha', and the chicken enzyme.";

J. BIOL. CHEM. 266:2362-2368(1991).

-!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFIPERERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCAS SUBSTRATES.

-!- FUNCTION: THE ALPHA AND ALPHA' CHAINS CONTAIN;

BETA CHAINS.

-!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, RETAINS CHAINS.
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KC21_HUMAN

ID KC21_HUMAN STANDARD;

AC P19138; P20426;

DT 01-NOV-1990 (REL. 16, CREATED)

DT 01-NOV-1990 (REL. 16, LAST SEQ
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collaboration
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RATTUS.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 1.
HSSP; P28523; 1A60.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BDOMAIN 39 324 PROTEIN KINASE.
NP_BIND 45 53 ATP (BY SIMILARITY).
BINDING 68 68 ATP (BY SIMILARITY).
ACT_SITE 156 156 BY SIMILARITY.
SEQUENCE 391 AA; 45143 MW; 559AA2A0 CRC32;
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ase II
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                                                                                                                                                                 Score 262; DB 1; Pred. No. 2.3e-09; Pred. No. 2.3e-09; Pred. Mismatches 125;
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31, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDAT
ALPHA CHAIN (CK II) (EC 2
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MEDLINE; 89323123.
MEISNER H., HELLER-HARRISON R., BUXTON
"Molecular cloning of the human casein
BIOCHEMISTRY 28:4072-4076(1989).
-!- FUNCTION: CASEIN KINASES ARE OPERAT
PREFERENTIAL UTILIZATION OF ACIDIC
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FUNCTION: THE ALPHA AND ALPHA'
SUBUNIT: TETRAMER COMPOSED OF
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26.5%;
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TISSUE=LIVER;
AHMED K., DAVIS A., HANTEN
GOUELI S.A.;
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                                                                                                                                                                                 Similarity 26.90; Conservative
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P19139;
01-NOV-1990 (REL.
01-FEB-1995 (REL.
15-JUL-1998 (REL.
CASEIN KINASE II, R
CSNK2A1.
RATTUS NORVEGICUS
EUKARYOTA; METAZOA,
RODENTIA; SCIUROGN
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BETA CHAINS
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                                                            EUTHERIA;
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a II.";
                                                                                                                                                                                                                                        C., TAKIO K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF C. SPECIES-BOVINE; TISSUE-TESLE.,
MEDLINE; 90237072.
LITCHFIELD D.W., LOZEMAN F.J., PIENING C., SOMMERCON WALSH K.A., KREBS E.G.;
"Subunit structure of casein kinase II from bovine 'Subunit structure of casein kinase II from bovine 'Demonstration that the alpha and alpha' subunits are polypeptides.";

J. BIOL. CHEM. 265:7638-7644(1990).
C.!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFICE PROFIEDS.
C.!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFICE PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCCESTRATES.
                                               TAURUS (BOVINE).
VERTEBRATA; MAMMALIA;
E; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from bovine 'subunits a
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ase II
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casein kinase
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                                                                                                                                          J., CZE
kinase
     UPDATE) (EC 2.7.
                                                                                                                                                                                                                                                                                                                                                              BROWN W.C., IAMS K.P., NAYAR
                                                                                             SEQUENCE FROM N.A.
SPECIES=HUMAN;
MEDLINE; 89323123.
MEISNER H., HELLER-HARRISON R., BUXTON J.
"Molecular cloning of the human casein ki
BIOCHEMISTRY 28:4072-4076(1989).
[2]
SEQUENCE FROM N.A.
SPECIES=HUMAN;
MEDLINE; 91070071.
LOZEMAN F.J., LITCHFIELD D.W., PIENING C.
KREBS E.G.;
"Isolation and characterization of human "Isolation and characterization of casein k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s.,
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    32, LAST ANNOTATION ALPHA CHAIN (CK II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OHIO
                                                                                                                                                                                                                                                               d characterization of alpha' subunits of ca 29:8436-8447(1990).
01-NOV-1995 (REL. 32, LAST ANNOTATE CASEIN KINASE II, ALPHA CHAIN (CK CSNK2A1 OR CK2A1.
HOMO SAPIENS (HUMAN), AND BOS TAURE EUKARYOTA; METAZOA; CHORDATA; VERTIPRIMATES; CATARRHINI; HOMINIDAE; HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES-BOVINE; TISSUE-TESTIS;
WATANABE M., YUGE M., MAEDA O.,
                                                                                                                                                                                                                                                                                                                                                                                        induction
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G177994;
G162777;
G611; -.
A30319.
A35838.
S21335.
A35206.
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SEQUENCE FROM N.A.
SPECIES=BOVINE;
MEDLINE; 93223703.
OLE-MOIYOI O.K., B.
MACKLIN M.D.;
"Evidence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                    transformed by parva.";
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BIOCHEMISTRY 29
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; CYPRININAE; CARASSIUS.
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                                                                                                                                                                                                                                                                                              38 DYQLVRKL-GRGKYSEVFEAINITNNEKVVVKILK---PVKKKKIKREIKILENLRGGPN
                                                                                                                                                                                                                                                                                                                                      --SRIPALVFEHVNNTDFKQ--LYQTL
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                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                    ; DB 1; I
2.3e-09;
ches 125;
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, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
N KINASE 2 (EC 2.7.1.-).
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                                                                                                                                                                                                                                    Score 262; DB
Pred. No. 2.3e
9; Mismatches
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                                                                    EMBL; L15618; G415716; -.

EMBL; J02853; -; NOT_ANNOTATED_CDS.

PIR; B30319; B30319.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PFAM; PF00069; pkinase; 1.

HSSP; P28523; 1A60.

TRANSFERASE; SERINE/THREONINE-PROTEIN KIN
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HIRAI T., YAMASHITA M., YOSHIKUNI SAKAI N., NAGAHAMA Y.;
"Isolation and characterization of the cell cycle regulator cdc2."
                                                                                                                                                                                                                                                       59;
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ilarity 26.5%;
Conservative 5
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53
68
156
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156
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TISSUE=OOCYTE;
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Matches 90
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BINDING
ACT_SITE
SEQUENCE
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ACTIVATES
                            CELL
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                            THE
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Level PS0010, PROSITE; PS0010, PROSITE; PS00108; PROSITE; PS00108; PROSITE; PS00101; PROTEIN_PROSITE; PS00101; PROTEIN_PROSITE; PS00101; PROTEIN_PROMINE-PROTEIN K11, PRAM; PF00069; pkinase; 1.

HSSP; P24941; IFIN.

TRANSFERASE; SERINE/THREONINE-PROTEIN K11, PROSPHORYLATION.

TOOMAIN 4 286 PROTEIN KINASE.

FT BINDING 33 33 ATP (BY SIMILARITY).

FT BINDING 33 33 ATP (BY SIMILARITY).

ACT_SITE 127 127 BY SIMILARITY.

ACT_SITE 127 127 BY SIMILARITY.

TOOLRES 14 14 PHOSPHORYLATION (BY SIMILARITY).

TOOLRES 15 15 PHOSPHORYLATION (BY SIMILARITY).

TOOLRES 160 PHOSPHORYLATION (BY SIMILARITY).

TOOLRES 15 15 DB 1; INC.

"A: 33998 MW; 9D4B9802 CRC32;

"A: 1.9e-09;

"A: 1.9e-09;

"A: 1.9e-09;
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                            OF
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.V. BIOL. 152:113-120(1992).

- FUNCTION: PROBABLY INVOLVED IN THE CONTINTERACTS WITH CYCLINS A, D, OR E.

- ENZYME REGULATION: PHOSPHORYLATION AT THE ENZYME, WHILE PHOSPHORYLATION AT THE SIMILARITY).

- SIMILARITY: WITH THE CONSERVED CATALYTICS.
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                                                                                                                                                 G., CHÜRCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH
IITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: NOT KNOWN. COULD FUNCTION IN ASSOCIATION WITH
MCS2.
                                                                                                 its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 306;
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EMBL; Z69239; E1188809; -.
PIR; S39151; S39151.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
HSSP; P24941; 1AQ1.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BII DOMAIN 17 25 ATP (BY SIMILARITY).
BINDING 40 40 ATP (BY SIMILARITY).
BINDING 40 40 ATP (BY SIMILARITY).
BINDING 40 ATP (BY SIMILARITY).
BINDING 40 ATP (BY SIMILARITY).
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CSK1 OR SPAC1D4.06C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE,
SCHIZOSACCHAROMYCES.
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                                                                                               fission yeast mcs2
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                                                                                                     protein kinase activity.";
EMBO J. 12:1723-1732(1993)
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                                                              SEQUENCE FROM N.A. MEDLINE; 93223713. MOLZ L., BEACH D.; "Characterization o
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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306
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STRAIN=972;
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SUBMITTED
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MEDLINE;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: AND WITH A CYCLIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY
PROTEIN KINASES.
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Pred. No. 2.4e-0
7; Mismatches 1
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LAST ANNOTATION UPDAT;
PROTEIN 2 HOMOLOG 3 ()
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TRANSFERASE; SERINE/THREONINE-PROTEIN KIN PHOSPHORYLATION.
DOMAIN 23 306 PROTEIN KIN ATP (BY SIM BINDING 52 52 ATP (BY SIM BINDING 52 33 33 PHOSPHORYLAM MOD_RES 33 33 PHOSPHORYLAM SEQUENCE 311 AA; 35047 MW; 6594D66E
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"A family of trypanosome cdc2-related FGENE 162:147-152(1995).
-! FUNCTION: PROBABLY INVOLVED IN THE -! - ENZYME REGULATION: PHOSPHORYLATION
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CD CC23_TRYBB
STANDARD;
AC P54666;
DT 01-OCT-1996 (REL. 34, CF)
DT 01-OCT-1996 (REL. 34, LA)
DT 01-OCT-1997 (REL. 35, LA)
DT 01-NOV-1997 (REL. 35, LA)
DE CELL DIVISION CONTROL PI
SN CRK3.
DS TRYPANOSOMA BRUCEI BRUCH
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36, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
ALPHA CHAIN (CK II) (EC 2.7
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-! FUNCTION: CASEIN KINASES ARE OPERATION PREFERENTIAL UTILIZATION OF ACIDIC PRO-
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MUS MUSCULUS (MOUSE).
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**BLOSUM62** Scoring table:

11428610 residues 119832 seqs, Searched:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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- AEMVN

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-KSAFPKWQAQD

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                                                                                        DDKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKD
                             KLPPKDEPPMAKY IDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVK
-DRRINALKLADFGLARAF
                                                                                                                                                                                                                                                                                                                                                                            FROM PNEUMOCYSTIS
                                                 Score 255.5; DB 2;
Pred. No. 1.4e-15;
); Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N---RSNCVRLLDILHAESKLYLVFEFLDMDLKKYMDRISE-
                                                                                                                          --KIFRVLGTPNEQSWPGVSSLPDY
                                                                                                                                                                                      283
  IKSYLYQILRGVAYCHSHRVLHRDLKPQNLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0
                                                                                                                                                         WDIILPRCNDDLMKEIFTKMIRYDRSKRITSKEILQ
                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07039/055001
                                                                                                                                                                                                                                                                                                                                                                                                                                           P.C., P.
E, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                  US-08-874-347-22

Sequence 22, Application US/08874347

Patent No. 5863741

GENERAL INFORMATION:

APPLICANT: Limper, Andrew H.

APPLICANT: Leof, Edward B.

APPLICANT: Thomas, Charles F.

APPLICANT: Gustafson, Michael P.

TITLE OF INVENTION: CARINII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIDKELIYNSAISDIYTAIDKFNNLPVCLK
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P
STREET: 60 South Sixth Street,
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 0703
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDALL
STREET: 60 SOLL
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
AMDIUM TYPE: Diskette
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Similarity 24.3%;
1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES
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                                                               GIPVRTFTH-
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Best Local
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    QIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDWDIILPRCNDDLMKEIFT
                                                                                                 - KPSFPKWARQDFSKVVPPLDED-GRSLLS
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                                      -AEMVTRRALFPGDSEIDQLF
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.larity 25.3%; Pred. No. 7.3e-16;
Conservative 60; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                  P.C., P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 Leof, Edwardes b.
Thomas, Charles b.
Gustafson, Michael P.
ENVENTION: CDC2 PROTEIN K
                                                                                                                                                                                                       RESULT 2
US-08-874-347-26
Sequence 26, Application US/08874347
Patent No. 5863741
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN K.
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Fish & Richardson P
: 60 South Sixth Street,
Minneapolis
                           |:|||::|| | :||||| | LWYRAPEILLGSKYYSTAVDIWSLGCIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26:
                                                                                         :|| :|| :|| :| :|
RIFRTLGTPDEVVWPGVTSMPDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                281
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LENGTH: 294 amino acid
TYPE: amino acid
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les 85; Conser
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MOLECULE TYPE: -08-874-347-26
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STREET: 60
CITY: Minr
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TELEX:
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Best Local S
Matches 85
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KIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANEIEEKDIKLW
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-NRPKYPGIKFEELFPDW-
                                                            -CYDLKLPPKDEP
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                                                                                                                                                               HVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPR-
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                                                          LKSMSSGLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDI
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Pred. No. 4.1e-15
; Mismatches 12
                                                                                                                                                                                                                   ---RCNDDLMKEIFTKMIRYDRSKRITSKEILO
                                                                                                                                                                                                                                           -IFPSESERDKIKTSQARDLLSKMLVIDPDKRISVDEALR
                                                                                                                                                                                                                                                                                                                                                                                                         KINASE
                                                                                                                                                                              --WNKVIEQLGTPS-AEFMKKLQPTVRNYVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                INC
                                                                                                                                                                                                                                                           sequence 2, Application US/08674612;
Patent No. 5663313;
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: A NOVEL HUMAN MAP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 0.1
                                                                                                                                                                                                                                                                                                                                                                                         Craig G. : A NOVEL HUMAN MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,612
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/674,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/000,722
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0036
TELEFHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           980
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                                EEFQDVYLVMELMDANLCQVIHM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sh 14.0%;
Similarity 26.4%;
91; Conservative
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                                                                                                                                                                                                                                                                                  RESULT 5
US-08-674-612-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 91
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-08-674-61
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KDEPPMAKYI-DVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDK
                                                                                --AEMIRRSP
                                                                                                       ELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDWDI
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                                                                                                                    Length
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                                                                                                                                                                                                                                                                         APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL APPLICANT: Karin, Michael APPLICANT: Bavis, Roger APPLICANT: Hibi, Masahiko APPLICANT: Lin, Anning APPLICANT: Derijard, Benoit TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                Score 255.5; DB 3;
Pred. No. 2.2e-15;
49; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: PCT/US94/08119
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: LISA A. HAILE, PH.D.
REGISTRATION NUMBER: FD-3205
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 18:
CENTENCE CHARPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      Lubitz
                                                                                                                                                            335
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                                                                                                                                                                        VVPNGEEDAI-ELLSAMLVYDPAHRISAKRALQ
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PCT-US94-12913A-18
Sequence 18, Application PC/TUS9412913A
GENERAL INFORMATION:
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RY: USA
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Local Similarity 27.1%;
nes 92; Conservative
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LENGTH: 424 amino acid
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PCT-US94-12913A
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CITY: I
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                                  KLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDF--SLPPHSIHREIFILKTL
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                                                                                                                                                                                                                                              174 DICYDLKLPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGII----LTGLY
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US-08-920-296-2
Sequence 2, Application US/08920296
Patent No. 5846778
GENERAL INFORMATION:
Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: A NOVEL HUMAN MAP KII
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
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Lucy J.
PER: 36,749
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FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
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STREET: 3174 Porter Drive
CITY: Palo Alto
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MEDIUM TYPE: Floppy
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No. 4.1e-15;
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Mismatches
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REFERENCE/DOCKET NUMBER: ATG50036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
TELEFAX: 610-270-5090
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,788
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,902
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/123,175
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: 08/250,975
FILING DATE: 31-MAY-1994
                                                           Score
Pred.
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,7
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Sequence 2, Application US/08746788

GENERAL INFORMATION:
APPLICANT: McDonnell, Peter
APPLICANT: Young, Peter
TITLE OF INVENTION: DRUG BINDING
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Correspondence of Prussia
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRUG BINDING
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Road
                                                                                      26;
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IBM Compatible
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                                                          14.0%;
26.4%;
                                                                          Similarity 26.491; Conservative
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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214915
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US-08-746-788-2
                                                           Query Match
Best Local S
Matches 91
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US-08-920-296
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Query Match
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ted Thereto
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Patent No. 5801015

GENERAL INFORMATION:

APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique

APPLICANT: Damagnez, Veronique

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

TITLE OF INVENTION: 4 Human Pathogens, and Uses Related The

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley, Hoag & Eliot, Lid

STREET: One Post Office S....

CITY: Boston

STATE: MA
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                                                                                                                                                                           ; DB 2;
..2e-14;
nes 126;
                                                                                                                                                                                                                                                                                             Score 246.5;
Pred. No. 1.2e
6; Mismatches
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05-JUN-1995
08: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090;
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                    56;
                                                                                                                                                                         13.8%; 26.1%;
 2
N FOR SEQ ID NO: 2
CHARACTERISTICS:
1: 365 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                               N-terminal
                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide; HYPOTHETICAL: NO; ANTI-SENSE: NO; FRAGMENT TYPE: N-termina; ORIGINAL SOURCE: US-08-746-788-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KTLFKGKDYLDQ---
                                                                                                                                                                                                    Conservative
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                                                 STRANDEDNESS
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US-08-463-090B-9
           SEQUENCE C
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INFORMATION
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Matches 9
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Patent No
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1.1e-
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APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 33000 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ^{\circ}
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13-JUN-1997
ION: 435
INFORMATION:
REFERENCE/DOCKET NUMBER: MIV(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (178 in mino acida in molecule TYPE: protein
US-08-463-090B-9
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34,813
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OPERATING SYSTEM: DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATIONAME: Ellinger, Mark
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORM
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les 88; Conser
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US-08-874-347-18
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INFORMATION FOR
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                                                                                                   LENGTH:
TYPE: a
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Best Local S
Matches 85
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                                                                                                                                                                         Length 317
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122;
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                                                                                                                                                                          Score 246; DB 2;
Pred. No. 1.1e-14
); Mismatches 12
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t, Suite
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBER: US/08/874,347
13-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KI
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08874347 Patent No. 5863741
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IBM Compatible
SYSTEM: DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          th 13.7%;
Similarity 25.8%;
88; Conservative
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                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acid
TYPE: amino acid
                                                                                                        single
                                                                                                                               protein
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SOFTWARE: FastSEQ
IRRENT APPLICATION I
                                                                                                      STRANDEDNESS: Sin
TOPOLOGY: linear
MOLECULE TYPE: prot
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GENERAL INFORMATION:
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CITY: Minne
STATE: MN
COUNTRY: US
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S-08-874-347-24
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Best Local S
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Pred. No. 3e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
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ADDRESSEE: Fish & Richardson P.C., P.
STREET: 60 South Sixth Street, Suite
CITY: Minneapolis
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
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                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
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Diskette
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LENGTH: 297 amino act
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TOPOLOGY: linear
MOLECULE TYPE: prote
S-08-874-347-24
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STATE: ML.
COUNTRY: US/
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Best_Local Similarity
Matches 85; Conser
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10036
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TOPOLOGY: un)
MOLECULE TYPE:
US-08-176-620A-16
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Best Local
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Pred. No. 4.6e-14;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIILPRCNDDLMKEIFTKMIRYDRSKRITSKEILQ
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Patentin Release #1.0, 1
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Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
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Cobb, Melanie H.
Yancopoulos, George I
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1155 Avenue of the
                                                                                                 23
                                                                                             SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CORRESPONDENCE ADDR
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                                                                                                                                                            MOLECULE TYPE: -874-347-23
                                                                                               INFORMATION FOR
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APPLICANT:
TITLE OF IN
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CITY: N
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128;
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                                           NUMBER: US/08/176,620A: 03-JAN-1994
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                                                                                                                                                   -123
APPLICATION NUMBEL.
FILING DATE: 03-JAN-1>-
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-1
TELECOMMUNICATION INFORMATION:
TELEYONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: single
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Pred.
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Sequence 16, Application US/08461985

Patent No. 5872006

GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Yancopoulos, George D.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Manuma Price of Invention of the Americal Street: New York
STATE: New York
STATE: New York
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M PC compatible
TEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
OPERATING SYSTEM: PC
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MOLECULE TYPE:
IS-08-176-620A-14
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                                                                                                                                                                                                                                                                                                                                          61;
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Pred. No. 5.6e-14;
); Mismatches 128;
   N
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SOFTWARE: Patentin Release #1.0, Version JRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   --LDENGLDLLSKMLIYDPAKRISGKMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIILPRCNDDLMKEIFTKMIRYDRSKRITSKEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds
1155 Avenue of the Americas
                                                                         APPLICATION NUMBER: US 08/176,620 FILING DATE: 03-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Cobb, Melanie H.
Yancopoulos, George
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APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family
                                                                                                                                                                                                                                                                                                                    / Match
Local Similarity 25.4%; Procal 85; Conservative 60;
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U.S.A.
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                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: unkr
MOLECULE TYPE: F
US-08-461-985-16
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US-08-176-620A-14
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CITY: Ne
STATE: N
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APPLICANT:
APPLICANT:
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                CURRENT
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--RMLVFDPAKRITAKEALE
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                                                                                                                                                                        .25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 236.5; DB 1;
Pred. No. 8.7e-14;
; Mismatches 125;
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                                                                                                                                                                          Version
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03-JAN-1994
08: 800
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ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,620A

FILING DATE: 03-JAN-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-123
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Sequence 14, Application US/08461985

Patent No. 5872006

GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Yancopoulos, George D.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Maj
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americal Color of Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SLPMYPAAPLEKMFPRVNPKGIDLLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
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Best Local Similarity 25.7%;
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSENFQSVLVKDDKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFK
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Pred. No. 8.7e-14;
52; Mismatches 125;
                                                                                                Version
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
FEGISTRATION NUMBER: 18,872
FELEFONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFONMUNICATION INFORMATION:
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

WOLECULE TYPE: protein
US-08-461-985-14
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.7%; P. Matches 90; Conservative 62;
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e C ; Search time 41.67 Seconds
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US-09-072-994-13 1019 1 ATGAAGTTGTCBCDTT score: Title: Perfect sc Sequence:

..TTACAATTAATGTTGGATTG 1019 ATGAAGTTGTCAGATTATTA.

IDENTITY\_NUC Scoring table:

residues 125096042 311585 seqs, Searched:

N\_Geneseq\_36:\* Database

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution. score gand is Pred.

	escription	albicans Cdk ac	kD subunit of	Sequence encoding	0 kD subunit of	$\overline{}$	ence of A	uman 3'a	odium var	uman 3' apolipop	ence encod	promoter	rbamoyl-phos	NPX30 xylanase c	nodium var-7	ding Pla	protein. Ne	r mitochond	inuation (1	it resis	tochondri	ou (5 o	purgdort	inuation (6 o	Outinuation (14	ontinuation ( alaria-enecif	SPECIFIC P Prooding	equence encodi	arbamoyl-phosph	Late2-82	uation (10	ecombinant bo	inant	ecombinant bo	ecombi	lasmodi	lostridium bot	ictyoste	ontin	orrelia burgd	Sequence encoding	lium bergh	Aspergillus nidula
SUMMARIES	Ţ	X27495	2413	47	24134	2120		3153	7288	3153	വ	0 2 4 4 4 4 4	5232	1348 1300 0	007/	7.4.T007.F	0440	10000000000000000000000000000000000000		) ( ) ( ) (	0.000 D	4000	20249	21209 21209	1 00010	90223	6047	0356	629	43360	2024	2628	8797	0000	2629	3313	3057	1/10 1/10	024	2025	20358	1.0	883
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ф	Query Match	86	-	•	•	-	•	•	•	•	•	•	•		•	•		-		•	•						-	_		_		_	-										
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DY 22-100-1199 (first entry)

DY 22-100-1199 (first entry)

DY 22-100-1199 (first entry)

DY 22-100-1199 (first entry)

E.albaces cdk activating kinase (cAk) ...

KW Protein Xinase cyclin-dependent Xinase activat...

KW Screening assay; fungicide: ss.

Candida albacas.

PR 11-A0G-199; FR-010287

PR 12-A0G-199; FR-010287

PR 12-A0G-1999; FR-010287

PR 12-A0G-1999; FR-010287

PR 12-A0G-1999; FR-010287

PR 12-A0G-1999; PR-010287

PR 12-A0G-1999; FR-010287

PR 12-A0G-1997; FR-010287

PR 12-A0G-1999; FR-010287

PR 12-A0G-1997

PR 
        Insulin-stimulated
Mutant insulin-sti
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: 50kD subunits
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prodn. of recombinant endonuclease in eg. Sa
Claim 1; Page 2; 4pp; Japanese.
The sequence given encodes the 50kD subunit
Findonuclease Scel can be mass produced from
                                                                                                                                                                                                                                                                                                                                                          024134 standard; DNA; 1671 BP.
024134;
09-NOV-1992 (first entry)
50 kD subunit of Scel.
Endonuclease Scel; PAGE; chromatography; ENSachromyces cerevisae.
Key
Location/Qualifiers
cds
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07-APR-1992.
21-AUG-1990; 219566.
21-AUG-1990; JP-219566.
(RIKA ) RIKAGAKU KENKYUSHO.
WPI; 92-164281/20.
P-PSDB; R22667.
ENS2 gene encoding 50kD subuprodn. of recombinant endonu
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   purified by denaturing
                                                                                                     :
expressed from the ENS2 gene. The 50kD subunit was purified treating Scel from eg. Sacchromyces IAM4274, and by denaturing protein and subjecting it to PAGE, or by chromatography on a phosphocellulose column.

Sequence 1671 BP; 769 A; 108 C; 113 G; 681 T;
                                                                               167
                                                                              Length
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0.00041;
ches 428;
                                                                            Ouery Match
Best Local Similarity (45.6%; Pred. No. 0.00
Matches 365; Conservative (0; Mismatches
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AC N60472;
DT 24-AUG-1991
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       Antigen
                                                                                                                                                                                                                                                                                              poly:peptide(s) having antigenicity of RESA or FIRA antigens of falciparum
Claim 4; Fig 1; 55pp; English.
The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA antigenicity suitable for providing protective immunity against Plasmodium falciparum malarial infections.
Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4590;
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    Surface
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198;
   Erythrocyte
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                                                                                                                                                                                                                                                                                       of RESA or
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PAGE; chromatography; ENS2
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Pred. No. 0.00
0; Mismatches
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   ected
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Location/Qualifier
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                                                              /Qual
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                                                                              6.5%;
ilarity 49.6%;
Conservative
   ring
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27-MAR-1986.
11-SEP-1985; 006960.
11-SEP-1984; AU-007067.
11-SEP-1985; AU-047326.
(HALL-) HALL INST MED RES.
Kemp DJ, Anders R, Coppel
WPI; 86-094065/14.
P-PSDB; P60569.
                                                                                                                                                                                                                           KED RES.
Coppel
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Sequence encoding the rin(RESA).
Malaria vaccine; antigen;
Plasmodium falciparum.
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Q24134 standar
Q24134;
09-NOV-1992 (
50 kD subunit
Endonuclease S
Sacchromyces c
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                          prodn. of recombinant endonuclease in eg. Sacchromyces IAM4274 stalm 1; Page 2; 4pp; Japanese.

The sequence given encodes the 50kD subunit of endonuclease Scel.

Endonuclease Scel can be mass produced from the 50kD subunits expressed from the ENS2 gene. The 50kD subunit was purified by treating Scel from eg. Sacchromyces IAM4274, and by denaturing the protein and subjecting it to PAGE, or by chromatography on a sequence 1671 BP; 769 A. 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTGATAAGTTTAATAACTTACCAGTATGTCTTAAAATAGTTGATGAAGATTTCAGTCT
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Pred. No. 0.0055;
; Mismatches 423;
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/label= Scel_50kD_s
1. .81
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07-APR-1992.
21-AUG-1990; 219566.
21-AUG-1990; JP-219566.
(RIKA ) RIKAGAKU KENKYUSHO.
WPI; 92-164281/20.
P-PSDB; R22667.
ENS2 gene encoding 50kD subu
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tes 340; Conservative
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159. .1586
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82. .158
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671

851

85121

914

85284

794

85344

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Example; Fig 13; 45pp; English.

A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungi is claimed. Prefit the DNA sequence codes for bovine preprochymosin, M. meihei preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which increases transformation efficiency, e.g. ANS-1.

Sequence 1864 BP; 786 A; 210 C; 44 G; 732 T;
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                                                                                                           GCATITITAAAAATICAATITACAAAATATCCTAGAAAAGATIGGGATATITITACC
                                        TTTGTTGTTTTTACTGATTGTAGATTTAGAGATGATGTTGTATCATTTAAAAAAATAGATAA
AGCAGAATTTTATAATTCAACATTTAAATCTCATGTATATTTTGATGATATATCATTTAA
                     TAATGATTCTCATGTTAGTGATTTATATTTAAATCAAATATTTGAAAATTTTCGGTAC
                                                                ACCCAATTTAACTGATTTTGAAGATGAATTATTTTGTGATGAATAATAATGAAAACTT
                                                                                    AGAAAATTTTAAAGGTTTAGCAAT - - - ATTCCTTAAAACTCAATTTCTAAACAAACACAC
                                                                                                                                AACGATAGAAAACTTCCAATTATCAAAACATCATTTTTAAAAACAGATGTTAGAGAAGT
                                                                                                                                                                                                                                                               transformation efficiency. Aspergillus expression vector
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 87-095049/14.
New DNA sequences for expressing polypeptide in filamentous for with secretion of prod. from the cells, and new vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1864;
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Pred. No. 0.03;
); Mismatches 532
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ANS-1 which increases
gal expression vector;
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ilarity 42.4%;
Conservative
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Mucor miehei.
EP-215594-A.
25-MAR-1987.
27-AUG-1986; 306624.
29-AUG-1985; US-771374.
07-JUL-1986; US-882224.
(GENE-) GENENCOR INC.
Cullen D, Gray GL, Hayengwel; 87-095049/14.
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Best Local Similarity
Matches 397; Conser
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N71405;
18-APR-1991 (fi
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                                              AAATTATTATAATATTTTTAATAATTCATTATATTTAATGAAATATTATTATTA
                                                                    GACTAATGATTCTCATGTTAGTGATTTATATTTAAATCAAATATTTGAAATTTCGG
                                                                                TTATCTATTAAAAAATTATTAGATAAATTAAGTTGAATATTAGATAGTTTATAATTT
                         TTTGACTGGTTTATATTCAGAAATTTTCAAAGTGTTTTAGTCAAAGATGATAAAGAATT
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Claim 7; Page 59-60; 84pp; English.
Human apolipoprotein B (apoB) scaffold attachment region (SAR) element clones Rh32 (T31530) and Rh10 (T31531) respectively carry the 3' human apoB SAR element and the distal 1212 bp 5' human apoB SAR elements
Co-map with the boundaries of the human apoB gene chromatin domain. A novel recombinant DNA molecule adapted for transfection
TAAATTATATAAAAATAGAAGTTATTATAAATATTTAATTTAGGTATTTAAANTAGGTAT
                                                     TTCATCGTGATATAAAACCCAGTAATATTTTCTTTGCCCGGGATGATATAACACAACCGA
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gene therapy; vector;
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Human 3' apolipoprotein B SAR
Erythropoietin; EPO; anaemia;
scaffold attachment region; SA
transgenic animal; SS.
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27-JUN-1996.
18-DEC-1995; CA0696.
19-DEC-1994; US-358918.
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                                                                                                                                     TTATTATATAGACAAGGAATTAATTTACAATAGTGCCATTTCTGATATATACGGCTAT
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of a host cell comprises an erythropoietin (EPO) cDNA (T31529) (genomic clone (T31532) operably linked to an expression control sequence and to the 5' and 3' SAR elements. The SAR elements increase expression of the recombinant EPO in stable, long-term mammalian cell cultures.

Sequence 605 BP; 278 A; 18 C; 35 G; 274 T;
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Pred. No. 0.046;
; Mismatches 199;
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Best Local Similarity 47.2%;
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gene family; SABP; sia]
y binding like gene; Du
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19-DEC-1996.
07-JUN-1996; U09508.
07-JUN-1995; US-487826.
(USSH ) US DEPT HEALTH & Chitnis C, Miller LH, E Wellems TE;
WPI; 97-052231/05.
P-PSDB; W22475.
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T72882;
12-SEP-1997 (first ent
Plasmodium var-7 gene.
DBL gene family; SABP;
Duffy binding like gene
DABP; merozoite; malari
Plasmodium; ss.
Plasmodium vivax.
Plasmodium falciparum.
Key
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Claim 4; Page 56-61; 96pp; English.

S claim 4; Page 56-61; 96pp; English.

This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and stalic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP carface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially right of the plasmodium merozoites (especially rights).
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Pred. No. 0.047;
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1 Similarity 45.2%;
464; Conservative
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Plasmodium falciparum or
Sequence 19124 BP;
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Best Local
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Recombinant DNA molecule expressing mammalian erythropoietin recombinant DNA molecule expressing mammalian erythropoietin recombinant DNA molecule expressing mammalian erythropoietin resecul lines, and for gene therapy, e.g. of anaemia and other red blood cell disorders

Claim 7; Page 59-60; 84pp; English.

Colaim 7; Page 59-60; Page 60; Page
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KW Erythropoietin; EPO; anaemia; gene therapy; vector;

KW scaffold attachment region; SAR element; apolipoprotein B;

KW transgenic animal; ss.

Homo sapiens.

NO9619573-A1.

DEC-1995; CA0696.

R 19-DEC-1994; US-358918.

A (CANG-) CANGENE CORP.

I Delcuve G;

WPI; 96-30057-
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Local Similarity 46.3%;
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AATTATGAATATGAAATTGATATTTGGTCATTGGGTATAATTTTGACTGGTTTATATTCA
                                                           AGTGATTTATTATTAAATCAAATATTTGAAAATTTCGGTACACCCAATTTAACTGAT
                                                                                                                       TTTGAAGATGAATTATTTTGTGATGAATATAATAATGAAAACTTGCATTTTAAAAATTC
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The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the nev DNA sequence, together with a carrier.

Sequence 5760 BP; 2565 A; 630 C; 725 G; 1840 T;
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Pred. No. 0.082;
0; Mismatches 3
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11-SEP-1985.
21-FEB-1985; 301173.
22-FEB-1984; GB-004692.
26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
(WELL ) WELLCOME FOUNDATION LTHOlder A, Sandhu J, Odink K, LWPI; 85-224845/37.
P-PSDB; P50777.
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Malaria vaccine; epitope; an
Plasmodium falciparum.
Key
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Best Local Similarity 44.5%;
Matches 276; Conservative
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Claim 2; Fig I
The sequence (
(N50530) and (
(see P50777)
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N50530;
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Malaria vacc
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Lin S;

WPI; 99-080895/07.

New transgenic fish - containing cells which contain an ornstruct comprising homologous expression sequences which direct construct comprising homologous expression product

Cell-specific expression of an expression product

Calim 13; Page 54-57; 69pp; English.

Craim 6ATA-1 (X08941) and GATA-2 (X08942) transcription factors are reteprized in processed in specific can be specific transcription factor. These transgenic can be used in plasmid constructs also comprising an expression product.

Craim 6ATA-1 (X08941) and 6ATA-2 (X08942) transgenes.

Craim 6ATA-1 (X08941) and 6ATA-1 (X0894
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X08941;
X08941;
27-APR-1999 (first entry)
GATA-1 promoter region.
GATA-1; GATA-2; zebrafish; transgenic a expression; developmental process; line transcription factor; transcription; ds Brachydanio rerio.
W09856902-A2.
17-DEC-1998.
09-JUN-1998; U11808.
09-JUN-1999; U2-871755.
(MEDI-) MEDICAL COLLEGE GEORGIA RES INS
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Similarity

Query Match Best Local

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23-DEC-1993.
17-JUN-1992; AU-002985.
29-JUN-1992; AU-003238.
01-APR-1993; AU-008100.
(CSIR ) COMMONWEALTH SCI & Xue GP; WPI; 94-007529/01.
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P-PSDB; R44529.
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PD 09-7UN-1994.

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PD 09-7UN-1994.

PEC-1992; AU-006206.

PR 16-DEC-1992; AU-006380.

PR 16-DEC-1992; AU-006380.

PR 194-200271/24.

PR 194-200271/24.

PR PETCREA MV. Osullivan WJ, Stewart TS;

PR PETCREA MV. Osullivan WJ, Stewart TGAATTWAATCA ALL

The Glutaniase subdomain of the glutanine-anidorransferase subdomain and creation of the glutanine-anidorransferase subdomain of the glutanine-anidorransferase subdomain of the glutanine-anidorransferase subdomain of the glutanine-anidorransferase subdomains of the second separates 2 AFP binding subdomains of the Sp20 BP; 3836 A; 774 C; 1232 G; 3078 T;

R920 BP; Score 56.2; DB 1; Length 8920;

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Carbamoyl-phosphate-synthetase
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claim 9; Figure 3; 45pp; English.

The cloned xylanase coding sequence is derived from an anaerobic rumen fungus. The xylanase has high specific activity for the hydrolysis of xylan. It can be used for treating pulps in the pul hydrolysis of xylan. It can be used for treating pulps in the pul and paper industry, for treating bagasse for more efficient dispos or for the treatment of feedstock to improve nutritional value. Genetically modified xylanase genes can also be used for the modification of rumen bacteria to improve plant fibre utilisation
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feedstock; rumen; plant fibre;
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12-SEP-1997 (first entry)
Plasmodium var-7 gene.

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-7; immune response;
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19-DEC-1996.
07-JUN-1996; U09508.
07-JUN-1995; US-487826.
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This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and stalic acid binding protein (SABP) conserved regions (see sepectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding C Plasmodium infected erythrocytes. SABP and the Duffy antigen binding C Plasmodium infected erythrocytes. SABP and the Duffy antigen binding C Supernatant after infected erythrocytes release merozoites. DABP and SABP CC mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the Sarasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and compositions are used for the treatment and prevention of malaria. They genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially Sequence 19124 BP), 7824 n.
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T41852;
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CDNA encoding Plasmodium falciparum erythrocyte membrane protein; malaria;
Plasmodium falciparum; erythrocyte membrane protein; parasite; SS.
detection; identification; treatment; prevention; parasite; SS.
Plasmodium falciparum MC type.
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New Plasmodium falciparum erythrocyte membrand develop products for the diagnosis, treatment malaria parasite infections
Disclosure; Figure 12; 149pp; English.
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(AFFY-) AFFYMAX TECHNOLOGIES NV.
Baruch DI, Howard RJ, Pasloske BI
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A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMP1) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the PfEMP1 protein of the MC type of Plasmodium falciparum. An alternative, truncated version of the coding sequence (a cDNA clone) c is given in T41853.
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**BLOSUM62** Scoring table: 122810 seqs, 40065486 residues Searched:

Database

PIR\_60:\*
1: pir1:\*
2: pir2:\*
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384 2 S71098 427 2 S71099 350 2 B35838 424 2 S13934 427 2 JC5694 294 2 JQ2243	ALIGNMENTS	n kinase (EC 2.7.1) - ; inase; protein SPAC24B11 omyces pombe uence_revision 13-Mar-199 930; S62551; S68433 K.; Murakami, H.; Stett3 1996 mediated by a Hog1-like N 75	Library, June 1995  PPases dephosphory  (89262; NID:9897809; PI	67757; NID:g1061288; P 1 linked to extracellu ; MUID:96107317 luence not shown 739; NID:g1022684; PID	ated transforming proteirotein; phosphotransferakinase homology <kin>inase ATP-binding motifhate (Thr) (covalent) #shate (Tyr) (covalent) #s</kin>	; ; ; :- SA YF
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C; Accession: S56225
R; Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T. submitted to the EMBL Data Library, May 1995
A; Description: Analysis of the nucleotide sequence of A; Reference number: S56186
A; Reference number: S56186
A; Accession: S56225
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A; Accession: S56225
A; Cross-references: EMBL:D50617; NID:g836685; PID:d10
C; Genetics:
A; Gene: SGD:CAK1
A; Cross-references: SGD:S0001865; MIPS:YFL029c
A; Map position: 6L
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E; Tang, L.; Pelech, S.L.; Berger, J.D. Biochim. Biophys. Acta 1265, 161-167, 1995 A; Title: Isolation of the cell cycle control generate number: S53538; MUID:95210349 A; Reference number: S53538; MUID:95210349 A; Residues: preliminary A; Molecule type: DNA A; Residues: 1-308 <TAN> A; Residues: 1-308 <TAN> A; Genetic code: SGC5 C; Genetic code: SGC5 C; Genetic code: SGC5 C; Reywords: ATP; phosphotransferase F; 7-262/Domain: protein kinase ATP-binding moti F; 38, 56, 133, 135/Active site: Lys, Glu, Asp, Lys
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Superfamily: kinase-related transforming protein; protein
Keywords: ATP; phosphoprotein; phosphotransferase; serine,
8-257/Domain: protein kinase homology <KIN>
16-24/Region: protein kinase ATP-binding motif
39,55,129,131/Active site: Lys, Glu, Asp, Lys #status prec
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protein kinase (EC 2.7.1.37) cdc2 homolog - slime molc C; Species: Dictyostelium discoideum C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #te C; Accession: $24386
R; Michaelis, C.; Weeks, G.
Biochim. Biophys. Acta 1132, 35-42, 1992
A; Title: Isolation and characterization of a cdc2 cDNP A; Reference number: $24386; MUID:92379089
A; Accession: $24386
A; Estus: preliminary
A; Molecule type: mRNA
A; Residues: 1-296 <MIC>
A; Cross-references: EMBL: M80808; NID:9167685; PID:9167
C; Superfamily: kinase-related transforming protein; pr C; Superfamily: kinase-related transforming protein; pr C; Superfamily: phosphoprotein; phosphotransferase; $F; 8-257/Domain: protein kinase homology <KIN>
F; 16-24/Region: protein kinase ATP-binding motif F; 39, 55, 129, 131/Active site: Lys, Glu, Asp, Lys #statu
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hypothetical protein YFL029c - yeast (Saccharomyces C; Species: Saccharomyces cerevistae C; Species: Saccharomyces cerevistae C; Date: 02-Sep-1995 #sequence_revision 19-Oct-1995
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Pred. No. 1.5e-10;
9; Mismatches 125;
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                                                                                                                          NIIEYFNDLKIYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANE
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Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asional kinase (EC 2.7.1.37) cdk2 - African clawed frog Nalternate names: cell division control protein CDC2 homolog Eg1 C. Species: Xenopus laevis (African clawed frog) C. Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change OG C. Accession: A37871; S15866; I51662; S14410 #text_change OG C. Accession: A37871; S15866; I51662; S14410 for Guellec, K.; Omilli Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991 #text_change OG A. Ritle: Cloning by differential screening of a Xenopus cDNA codir A. Reference number: A37871; MUID: 91126051 A. Molecule type: mRNA A. Residues: 1.297 PARA-A. Residues: 1.297 PARA-A. Residues: 1.297 PARA-A. Molecule type: mRNA A. Residues: 1.297 PARA-A. Molecule type: mRNA A. Residues: 1.297 PARA-A. Molecule type: mRNA A. Residues: 1.92, R. 94-297 CLEA-A. Molecule type: mRNA A. Residues: 1.92, R. 94-297 CLEA-A. Molecule type: mRNA A. Residues: 1.92, R. 94-297 CLEA-A. Molecule type: mRNA A. Residues: 1.93, R. 94-297 CLEA-A. Molecule type: mRNA A. Residues: 1.93, R. 94-297 CLEA-A. Molecule type: mRNA A. Residues: 1.93, R. 1994 A. Molecule type: MRL: MID: 95129896 A. Molecule type: MRL: MID: 95129896 A. Molecule type: DNA A. Reference number: 15162; MUID: 95129896 A. Molecule type: DNA A. Reference number: 15162; MUID: 95129896 A. Molecule type: DNA A. Residues: 1.39 coll.>A. Reference number: 15162 A. Molecule type: DNA A. Residues: 1.39 coll.>A. Reference and functions A. Residues: 1.25 Conetics: Molecule type: DNA A. Residues: 1.25 Conetics: Molecule type: DNA A. Residues: 1.25 Conetics: Molecule type: Molecule type: DNA A. Residues: 1.25 Conetics: Phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphores of the Menology KIN> F:10-18/Region: protein kinase Arr-Dinding motif F:1
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Score 265; DB 2; Pred. No. 7e-11; hismatches 123;
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Pred. No. 7.8e-11,
99; Mismatches 12.
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26.4%;
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Residues: 1-391 <MAR>
Residues: 1-391 <MAR>
Cross-references: GB:M59456; GB:J05736; NID:g211533; PID:g211534
Cross-references: GB:M59456; GB:J05736; NID:g211533; PID:g211534
Superfamily: kinase-related transforming protein; protein kinase homology <KIN>
37-299/Domain: protein kinase homology <KIN>
45-53/Region: protein kinase ATP-binding motif
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serine/threonine-specific
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                                                                                                                                                               B30319

Casein kinase II (EC 2.7.1.-) alpha chain - rat (fragment)

C; Species: Rattus norvegicus (Norway rat)

C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990.#text_change 28-

C; Accession: B30319

R; Meisner, H; Heller-Harrison, R; Buxton, J; Czech, M.P.

Biochemistry 28, 4072-4076, 1989

A; Title: Molecular cloning of the human casein kinase II alpha-subu

A; Reference number: A90543; MUID:89323123

A; Accession: B30319

A; Molecule type: mRNA

A; Residues: 1-384 <MEI>

C; Superfamily: kinase-related transforming protein; protein kinase

C; Superfamily: heterotetramer; phosphotransferase; serine/threoni

F; 30-292/Domain: protein kinase homology <KIN>

F; 38-45/Region: protein kinase ATP-binding motif
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C; Species: Gallus gallus (chicken)
C; Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #t(C; Accession: A38611
R; Maridor, G.; Park, W.; Krek, W.; Nigg, E.A.
J. Biol. Chem. 266, 2362-2368, 1991
A; Title: Casein kinase II. cDNA sequences, developmenta; Reference number: A38611; MUID: 91115855
A; Accession: A38611
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-391 < MAR>
A; Residues: 1-391 < MAR>
C; Superfamily: kinase-related transforming protein; plc; Superfamily: heterotetramer; phosphotransferase; S; 37-299/Domain: protein kinase homology <KIN>
E; 45-53/Region: protein kinase ATP-binding motif
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C; Species: Bos primigenius taurus (cattle)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C; Accession: S21335, A35206
R; Watanabe, M.; Yuge, M.; Maeda, O.; Ohno, S.; Kawasaki, H.; Suzusubmitted to the EMBL Data Library, October 1990
A; Description: Nucleotide sequence of CDNA for casein kinase II & A; Reference number: S21335
A; Molecule type: mRNA
A; Residues: 1-391 <WAT>
A; Biol. Chem. 265, 7638-7644, 1990
A; Liter Subunit structure of casein kinase II from bovine testis A; Reference number: A35206; MUID:90237072
A; Residues: 50-59;103-122;230-239;248-279;284-303 <LIT>
C; Superfamily: kinase-related transforming protein; protein kinase homeler: F; 37-299/Domain: protein kinase homeler: F; 45-53/Region: A27, Residues: exercity finase homeler: Right Residues: Res
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Pred. No. 1.5e-10;
9; Mismatches 125;
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NiAtternate manas: E21 homolog; protein kinase p34
C.$pecies: Homo saplens (man)
A.$pecies: Macad. Sci. U.S.A. 88, 2006-9010, 1991
A.$pecies: Homo mimber: A41227; MUID:92020980
A.$pecies: Manaper: A41227; MUID:92020980
A.$pecies: Homo saplens (manapers)
A.$pecies: Homo saplens (
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YHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASMIFRKEPF------
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                        Score 262; DB 2; Pred. No. 1.5e-10; Mismatches 125;
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Similarity 26.5%;
90; Conservative
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-AEMVTRRALFPGDSEIDQLF-
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cmatches 119;
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Pred. No. 1.2e-10;
; Mismatches 111
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                                                  Score 262; DB
Pred. No. 1.1e
9; Mismatches
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sequence extracted from NCBI backbone
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R; Hiral, T.; Yamashita, M.; Yoshikuni, M.; To Dev. Biol. 152, 113-120, 1992
A; Title: Isolation and characterization of go A; Reference number: A44878; MUID:92331802
A; Accession: A44878
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-298 <HIR>
A; Cross-references: GB:S40289; NID:g251619; P
A; Experimental source: oocyte
A; Note: sequence extracted from NCBI backbone C; Genetics:
A; Gene: cdk2
C; Superfamily: kinase-related transforming pr
C; Keywords: ATP; cell cycle control; mitosis; F; 2-255/Domain: protein kinase homology <KIN>F; 10-18/Region: protein kinase ATP-binding mo F; 33,51,127,129/Active site: Lys, Glu, Asp, L
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-REISLLKEMN-
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C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_cha
C; Accession: S36619
R; Smith, G; Mottram, J.
Submitted to the EMBL Data Library, August 1993
A; Description: A family of CDC2-related kinases in Trypanoso
A; Reference number: S36607
A; Reference number: S36607
A; Residues: 1-311 <SMI>
A; Residues: 1-311 <SMI>
A; Residues: 1-311 <SMI>
C; Superfamily: kinase-related transforming protein; protein
C; Superfamily: kinase-related transforming protein; protein
C; Keywords: ATP; phosphotransferase
F; 21-275/Domain: protein kinase homology <KIN>
E; 29-37/Region: protein kinase ATP-binding motif
F; 52, 70, 145, 147/Active site: Lys, Glu, Asp, Lys #status prec
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smatches 123;
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9; Mismatches
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   A; Title: Isolation and characterization of cDl A; Reference number: A40444; MUID:91195354 A; Accession: A40444 A; MUID:91195354 A; Accession: A40444 A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-294 <COL> A; Cross-references: GB:M60526 C; Superfamily: kinase-related transforming proc; Keywords: ATP; phosphotransferase C; Keywords: ATP; phosphotransferase F; 2-256/Domain: protein kinase homology <KIN> F; 10-18/Region: protein kinase ATP-binding mo F; 33,51,127,129/Active site: Lys, Glu, Asp, L
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C; Species: Schizosaccharomyces pombe
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_(C; Accession: S39151
R; Molz, L.; Beach, D.
EMBO J. 12, 1723-1732, 1993
A; Title: Characterization of the fission yeast mcs2 cyclin A; Reference number: S35380; MUID: 93223713
A; Accession: S39151
A; Molecule type: DNA
A; Residues: 1-306 <MOL>
A; Cross-references: GB: S59896; NID: 9299548; PID: 9299549
C; Genetics:
A; Gene: cskl
A; Introns: 168/3; 240/3
C; Superfamily: protein kinase homology
C; Keywords: serine/threonine-specific protein kinase
F; 9-268/Domain: protein kinase homology <KIN>
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Sci. U.S.A. 88, 3377-3381,
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N;Alternate names: stress-activated protein kinase
C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 10-Jul-1998
C;Accession: JC5531
R;Ishikawa, T.; Nakada-Moriya, Y.; Ando, C.; Tanda, N.; Nishida, S.; Minatogawe Biochem. Biophys. Res. Commun. 234, 489-492, 1997
A;Title: Expression of the JNK2-alphal gene in the developing chick brain.
A;Accession: JC5531; MUID:97320448
A;Accession: JC5531
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-382 <1SH>
A;Kesidues: 1-382 <1SH>
A;Cross-references: DDBJ:AB000807; NID:g1816447; PID:d1019937; PID:g1816448
C;Comment: This enzyme is involved in development of the central nervous system actors. It plays a role in the differentiation of central nervous system.
C;Genetics:
A;Gene: JNK2-alphal
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology <KIN>
F;24-278/Domain: protein kinase homology <KIN>
F;230/Active site: His #status predicted
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in unordered pieces.

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AL034419.10 GI:4995265
HTG3.PHASE1.
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

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contaminated with foreign sequence from E.coli, yeast, phage etc. Order of segments is not known; 800 n's segments. Unfinished: dJ1108D11 Contig_ID: 03938 acc Length: 168935 bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequen as soon as it is available and the accession number be preserved.
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2 (bases 1 to 187544)
Hyman, R.W., Qin, F., Fung, E.L., Condirect Submission
Submitted (19-FEB-1998) Stanford Dicenter, Stanford University, 855 C. 94304, USA
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malaria parasite P. falciparum.
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Hyman, R.W., Fung, E.L., Qin, F., Ta
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Plasmodium falciparum 3D7 chromosor Unpublished

(bases 1 to 104992)

Hyman, R.W., Qin, F., Fung, E.L., Conv. Direct Submission

Submitted (21-AUG-1998) Stanford Dicenter, Stanford University, 855 Ca 94304, USA

On Apr 2, 1999 this sequence versic NOTE: This is a 'working draft';
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Enkaryota, Alveolata, Apicomplexa, Haemosporida; Plasmodium.

Eukaryota, Alveolata, Apicomplexa, Haemosporida; Plasmodium.

E 1 (bases 1 to 14867)

S Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.

Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,

Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,

Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,

Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L.

Chromosome 2 sequence of the human malaria parasite Plasmodium

L Science 282 (5391), 1126-1132 (1998)

E rratum:[[published erratum appears in Science 1998 Dec

4;282(5395):1827]]

E 2 (bases 1 to 14867)

S Gardner, M.J.

Direct Submission

L Submitted (02-NOV-1998) The Institute for Genomic Research, 9712

Medical Center Drive, Rockville, MD 20814, USA

Location/Qualifiers

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P.falciparum complete gene map of plastid-like DNA (IR-B).

N x95276

91171591

X95276.1 G1:1171591

ED16 gene; rps1 gene; rps12 gene; rps3 gene; rps13 gene; rps14 gene; rps14 gene; rps14 gene; rps12 gene; rps17 gene; rps19 gene; rps16 gene; rps1 g
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3 (bases 1 to 14001)

S wilson, R.J.M.

Direct Submission

L Submitted (23-JAN-1996) R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London NW7 1AA, UK

Related sequences x90351-x90354 (incl.), and x87630-x87631 (in Location/Qualifiers

14001

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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished

* as soon as it is available and the accession r
                                                       Homo sapiens
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Eutheria; Primates; Catarrhini; Hominidae;
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AC004157.3 GI:4558582
HTG; HTGS_PHASE1.
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa;
1 (bases 1 to 187544)
Hyman, R.W., Fung, E.L., Qin, F., Tama and Davis, R.W.
Plasmodium falciparum 3D7 chromosom Unpublished
2 (bases 1 to 187544)
Hyman, R.W., Qin, F., Fung, E.L., Conw Direct Submission
Submitted (19-FEB-1998) Stanford DN Center, Stanford University, 855 Ca 94304, USA
On Apr 2, 1999 this sequence version
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/db_xref="taxon:5833"
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ATG: HTGS_PHASE1.

Malaria parasite P. falciparum.

M Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; P

1 (bases 1 to 104992)

Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., Kurdi,O. and Davis,R.W.

Plasmodium falciparum 3D7 chromosome 12

Unpublished

2 (bases 1 to 104992)

Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Dav Direct Submission

Submitted (21-AUG-1998) Stanford DNA Sequencing an Center, Stanford University, 855 California Avenue 94304, USA

On Apr 2, 1999 this sequence version replaced gi:4

* NOTE: This is a 'working draft' sequence. It cur

* consists of 3 contigs. The true order of the pie

* is not known and their order in this sequence re

* architerum.
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Homo sapiens Chromosome Unpublished

and Roe, B

Zhan, M.

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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Eukaryota; Eutheria; P

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SOURCE

Norman

ent Of Chemistry And Biochemistry Parrington Oval, Room 208, Norma

Zhan, M. and kc.,

Zhan, M. and kc.,

Direct Submission

Bubmitted (02-JUN-1999) Departm.

The University Of Oklahoma, 620 Parring.

The University of Oklahoma, 620 Parring.

Ok 73019, USA

On Jun 10, 1999 this sequence version replaced gi:49602.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 5 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* soon as it is available and the accession number will

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RESULT

DEFINITION

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GI:5032328

VERSION KEYWORDŞ

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FEATURE

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AJ223323
92879886
AJ223323.1 GI:2879886
transfer RNA-Asn; transfer RNA-Met; transfer RNA-Gene; tRNA-Met gene; tRNA-Tyr gene.
baker's yeast.

Mitochondrion Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetaceae; Saccharomycetaceae; Saccharomycets.

1 (base& 1 to 1867)
Francisci, S.
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Francisci, S.
Direct Submission
Submitted (05-FEB-1998) F
Developmental Biology, Un
00185, ITALY
2 (bases 1 to 1867)
Pistilli, D.
Thesis (1997) Dept. of Ce
Rome I, Rome, ITALY
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Pred. No. 0.0064;
0; Mismatches 469;
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FTILRYMFYNGRVKIVPNNLYDLLNYESLAHMIMCDGSFVKGGGLYLNLOSFTTKELI
FIMNILKIKFNLNCTLHKSRNKYTIYMRVESVKRLFPMIYKYILPSMRYKFDIMLWOK
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YNDPNFKRMKYVRYADDILIGVLGSKNDCKMIKRDLNNFLNSLGLTMNEEKTLITCAT
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YSCVLTLASKYRLKTMSKTIKKFGYNLNIIENDKLIANFPRNTFDNIKKIENHGMFMY
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ISHDLIIKELKRYISDKGFIDLVYKLLRAGYIDEKGTYHKPMLGLPQGSLISPILCNI
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Direct Submission

Direct Submission

Submitted (16-DEC-1998) Data collected by MIPS on behalf of the Submitted (16-DEC-1998) Data collected by MIPS on behalf of the European yeast mitochondrial genome sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152

Martinsried, Germany; E-mail: Mewes@mips.biochem.mpg.de

Location/Qualifiers

1. .85779

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/db_xref="taxon:4932"
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Mitochondrion Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 85779)
Foury, F., Roganti, T., Lecrenier, N. and Purnell,
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FEBS Lett. 4
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malaria parasite P. falciparum.

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

E 1 (bases 1 to 86829)

Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and Barrell, B.

Direct Submission

L Submitted (15-APR-1999) P. falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

On Mar 24, 1999 this sequence version replaced gi:4034877.

For more information about this sequence or the Malaria Project.
                       TATCGTTATGATTTGAGTCAATTGATTGAAATTACAAAATATTGTAAACGAACAACACGA
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see http://www.sanger.ac.uk/Projects/P_falciparum. IMI sequence is not the entire insert of clone MAL3P5. It shorter because we only sequence overlapping sections longer because we arrange for a small overlap between
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Saccharomyces douglasii mitochondrial tRNA-Ser a
partial sequence, and Varip (vari) gene, mitocho
encoding mitochondrial protein, complete cds.
U49822
g1236920
U49822.1 GI:1236920
mitochondrial tRNAser; vari; mitochondrial tRNAp
baker's yeast.

Mitochondrion Saccharomyces douglasii
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; S
accharomycetaceae; Saccharomyces.

1 (bases 1 to 1655)
Cardazzo,B., Pellizzari,R. and Carignani,G.
Characterization of the mitochondrial genome of
analysis of the vari gene
Unpublished

2 (bases 1655 to 2426)
Cardazzo,B., Rinaldi,T., Frontali,L., Carignani,
Evolution of the mitochondrial genome in yeast:
mitochondrial divergence in the two closely rela
S.douglasii and S.cerevisiae
Unpublished
3 (bases 1 to 2426)
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Dictyostelium discoideum.

Eukaryota; Dictyosteliida; Dictyostelium.

1 (bases 1 to 610)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshio, Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stagedevelopment

DNA Res. 5 (6), 335-340 (1998)

99156227

On Jan 19, 1998 this sequence version replaced gi:2150975.
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/db_xref="taxon:44689"
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Bombyx mori

Bombyx mori

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glos

Ditrysia; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 488)

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda, Setablishment of cDNA database of Bombyx mori

Unpublished (1999)
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                                                                   Dictyostelium
                                                                                                                                                                                      Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
Email: d402hu@sakura.cc.tsukuba.ac.jp.
Location/Qualifiers
1. .519
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyosteli
1 (bases 1 to 519)
Yoshino, R., Morio, T. and Tanaka, Y.
Developmental cDNA in Dictyostelium di
Unpublished (1997)
On Jan 19, 1998 this sequence version
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/map="853A07; 17; 17q11.2-q
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/clone=lib="Dictyostelium d
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a 64 c 33 g 176 t
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Pred. No. 3.7;
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Matches 136; Conservative
GI:3060408
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Pterygota; Neoptera; Endopterygota; Diptera; Brachy
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 705)
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Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J.,
Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced.
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clone GH14939 5prime similar
Jaster complete mitochondrial
    replaced
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231 t
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                 Contact: Mita K
Genome Research Group
National Institute of Radiological Sci-
Anagawa 4-9-1, Inage, Chiba 263-8555,
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
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/db_xref="taxon:7091"
/clone="fbf0818f"
/clone_lib="Bombyx mor:
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/db_xref="taxon:7227"
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/clone="GH14939"
/clone_lib="GH Drosophila melanogaster head pOT2"
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/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
xhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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                                                   est@fruitfly.berkeley.edu
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h quality sequence stop: 582.
Location/Qualifiers
1. .705
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University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, Fax: 510 643 9947

Email: http://www.fruitfly.org/ES/Plate: 149 row: D column: 3

High quality sequence stop: 582.
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/clone_"SWOv3MCAM25C06"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3)"
/dev_stage="molting L3"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
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Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
                                <u>L3</u>
                                                                                                                                                                                                                                                                 version replaced
                             volvulus molting Livolvulus cDNA clone
                                                                                                                                                                       Secernentea;
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Eukaryota; Metazoa; Nematoda; Secernentea;
Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 1145)
Williams, S.A., Lizotte-Waniewski, M., Lane;
Genes expressed in molting L3 larvae of Oi
Unpublished (1997)

On Mar 20, 1998 this sequence version rep
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/db_xref="taxon:6282"
/map="16"
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SWOv3MCAM25C06SK Onchocerca vc
(SL96MLW-OvmL3) Onchocerca vol
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AI581441
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AI581441.1 GI:4567336
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106 c 77 q
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Drosophila melanogaster cDNA clone LP07659 5prime similar to
U37541: Drosophila melanogaster complete mitochondrial genome, misequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insteryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insteryota; Neoptera; Endopterygota; Diptera; Brachycera Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced ga
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G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@
Plate: 76 row: E column: 11
High quality sequence stop: 623.
Location/Qualifiers
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/dev_stage="larvae-pupae"
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Dictyostelium discoideum.

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Eukaryota; Dictyosteliida; Dictyostelium.

I (bases 1 to 590)

Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development

DNA Res. 5 (6), 335-340 (1998)

S 99156227

On Jan 17, 1998 this sequence version replaced gi:2044007.
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Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Jap
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA pr
Location/Qualifiers
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/organism="Dictyostelium dis/strain="AX4"
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/map="12; 6, 12; 12, 4.81cR
/clone="SSD784"
/clone_lib="Dictyostelium d:/dev_stage="Slug"
/ dev_stage="Slug"
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Dictyostelium discoideum.

Dictyostelium discoideum.

Eukaryota; Dictyosteliida; Dictyostelium.

1 (bases 1 to 478)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H. Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage
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Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
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Pred. No. 6.8;
0; Mismatches
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/strain="AX4"
/db_xref="taxon:44689"
/map="2"
/clone="SLB603"
/clone_lib="Dictyostelium d
/dev_stage="slug"
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AA550575 755 bp DNA EST 11-AUG-1997 1740m3 gmbPfHB3.1, G. Roman Reddy Plasmodium falciparum genomic clone 1740m, mRNA sequence.
AA550575 92320827
    Dictyostelium
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Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA
Location/Qualifiers
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                                                                                             Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostel.
1 (bases 1 to 424)
Yoshino, R., Morlo, T. and Tanaka, Y.
Developmental cDNA in Dictyostelium diupublished (1997)
On Jan 14, 1998 this sequence version
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Pred. No. 7.6;
0; Mismatches
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/lab_host="E. coli XL1-Blue"
/note="Vector: pBlueScript SK(+); Genomic DNA, from
asynchronous blood stage parasites of the cloned Honduran
HB3 isolate cultured in vitro, was digested with mung bean
nuclease in the presence of 30% formamide at 50oc
(Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988.
Nucleic Acids Research 16:6883-6896). The ends of the
fragments were polished using T4 DNA polymerase, and the
fragments were ligated to EcoR V-cleaved and
dephosphorylated pBlueScript SK(+). Recombinant plasmids
transformed E. coli XL1-Blue."
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                                                                                   Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, I Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the Plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
97001675
On May 18, 1995 this sequence version replaced qi:811125.
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                                                             Apicomplexa;
                                                                                                                                                                                                                                Contact: Dame JB
Department of Pathobiology
University of Florida
2015 SW 16th Ave., Bldg. 1017, Grel: 352 392 4700
Fax: 352 392 9704
Email: dame@icbr.ifas.ufl.edu
Seq primer: T3.
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Location/Qualifiers
1. .755
/organism="Plasmodium f
/db_xref="taxon:5833"
                                 falciparum
 AA550575.1 GI:2320827
EST.
malaria parasite P. fal
Plasmodium falciparum
Eukaryota: Alveolata; A
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/clone="1740m"
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Oryza sativa.
Oryza sativa.
Oryza sativa.
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 712)

Yamamoto, K. and Sasaki, T.

Yamamoto, K. and Sasaki, T.

Rice cDNA from mature leaf
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3187085.
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CDNA
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/db_xref="taxon:4530"
/clone="S20934_1A"
/clone_lib="Oryza sativa mature latissue_type="mature leaf"
a 149 c 166 g 195 t
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/organism="Oryza sativ
                 mature le
sequence.
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National Institute of Agrobiolo
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
Ibaraki,
                                                                                                                                                                                                                                                                                                                                    Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT -'RGP'.
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712 bp
sativa
IA, mRNA
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Best Local Similarity 51.0%;
Matches 147; Conservative
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Dictyostelium discoideum.

SM Dictyostelium discoideum

Eukaryota; Dictyosteliida; Dictyostelium.

E 1 (bases 1 to 579)

SMORIO, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Yoshino, R., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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                                                                                                                                                                                                            Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/map="21q"
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Pred. No. 8;
0; Mismatches
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/clone_lib="Dictyostelium
/dev_stage="slug"
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                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapod Pterygota; Neoptera; Endopterygota; Lepidoptera; G Ditrysia; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 717)

Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maed Establishment of cDNA database of Bombyx mori Unpublished (1999)

On Oct 6, 1998 this sequence warried.
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Genome Research Group
National Institute of Radiological S
Anagawa 4-9-1, Inage, Chiba 263-8555
Email: kmita@uexs64.nirs.go.jp
PROJECT - 'CREST project by JST'.
Location/Qualifiers
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/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="e40883"
/clone_lib="Bombyx mori
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Ditrysia; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 593)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Establishment of cDNA database of Bombyx mori
Unpublished (1999)
On Oct 30, 1998 this sequence version replaced gi:3816581.
                                                                                                                                                                                                Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
1. :593
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/clone=lib="Bombyx mori p50(Daizo,)"
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Momestic silkworm.

Bombyx mori

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

Ditrysia; Bombycoidea; Bombycidae; Bombyx.

E 1 (bases 1 to 688)

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.

Establishment of cDNA database of Bombyx mori

Unpublished (1999)

On Oct 8, 1998 this sequence version replaced gi:3726239.
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Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
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/strain="p50(Daizo)"
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/map="8"
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US-08-605-106-4
US-08-544-332-8
US-08-526-964-2
US-08-602-010A-1
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US-08-46-855A-1
Sequence 1, Application US/08446855A
Sequence 1, Application US/08446855A
Patent No. 5849573
GENERAL INFORMATION:
APPLICANT: FLORES, Maria V
APPLICANT: FLORES, Maria V
APPLICANT: FLORES, Maria V
APPLICANT: PLORES: 2
CORRESPONDENCE ADDRES: 2
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE FORM:
MUMBER OF SEQUENCES: 2
CORRESPONDENCE FORM:
COUNTRY: USA
COUNTRY: USA
COMPUTER: PATENTE FORM:
MEDIUM TYPE: FLOREY disk
COMPUTER: PATENTIN RELEASE #1.24
COMPUTER: DATENTIN RELEASE #1.24
COMPUTER: DATENTIN BATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION NUMBER: 29.009
REGISTRATION NUMBER: 29.009
REGISTRATION NUMBER: 47-80
TELEFAN: 703-816-4100
TREERENCE/DOCKET NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
TELEFAN: 703-816-4100
TNFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
TYPE: nucledc acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
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Best Local Similarity 45.4%;
Matches 328; Conservative
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US-08-463-090B-5
Sequence 5, Application US/08463090B
Fatent No. 5801015
GENERAL INFORMATION:
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley, Hoag & Eliot, LLP
STREET: MA
COUNTRY: USA
COUNTRY: USA
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TAATCTTGTTAGTAATCAATATACACTTGCTAATGAAATTG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV032.01
TELECOMMUNICATION INFORMATION:
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US-08-526-964-1
Sequence 1, Application US/08526964
Patent No. 5698421
GENERAL INFORMATION:
APPLICANT: Lambowitz, Alan M
APPLICANT: Zimmerly, Steven
APPLICANT: Tang, Jian
ITTLE OF INVENTION: Nucleotide Integra
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
STATE: Ohio
COUNTRY: USA
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,964
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLICK, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           684
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TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1058
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                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                        Score 51.4; DB 2;
Pred. No. 0.013;
); Mismatches 396;
REFERENCE/DOCKET NUMBER: 22727/00127

TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-526-964-1
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il Similarity 45.5%;
338; Conservative
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Matches 338
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TOPOLOGY: linear

MOLECULE TYPE: cDNA

Sequence 1, Application US/08946617

Patent No. 5869634

GENERAL INFORMATION:

APPLICANT: Lambowitz, Alan M

APPLICANT: Zimmerly, Steven

APPLICANT: Guo, Huatao

APPLICANT: Yang, Jian

TITLE OF INVENTION: Nucleotide Integrase Preparation

TITLE OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calfee, Halter & Griswold
RESULT 4
US-08-946-617-1
Sequence 5, Application US/08911320A
Patent No. 5869633
GENERAL INFORMATION:
TILLE OF INVENTION:
THROMBIN RECEPTOR HOMOLOG
CORRESPONDENCES:
STREET: 3174 PORTER PHARMACEUTICALS, INC.
STREET: 3174 PORTER Drive
CITY: Palo Alto
STREET: GA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,320A
FILLING DATE:
APPLICATION NUMBER: US/08/911,320A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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NAME: GOLFICK, Mary E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: US/08/911,320A
FILING DATE: August 14, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,125
FILING DATE: 6-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0041-1 DIY
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/946,617
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RRENT APPLICATION DA
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CLASSIFICATION:
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TCTTAAAATAGTTGATGAAGATTTCAGTCTTCCACCACATTCAATCCATCGAGAAATTTT 161
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Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System NUMBER OF SEQUENCES: 66
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Pred. No. 0.024;
); Mismatches 156;
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, Bt
CITY: Arlington
STATE: Virginia
COUNTRY: USA
21P: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
TELEPHONE: 703-816-4000
TELEPHONE: 703-816-4100
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
CENCENT OF PASSON DATES
                               sequence esynthetase
               livan, william C
N: Nucleotide s
N: phosphate sy
SS: 2
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Best Local Similarity 48.0%;
Matches 144; Conservative
APPLICANT: Flores, Maria APPLICANT: O'Sullivan, TITLE OF INVENTION: Nucritative of INVENTION: phonomer of Sequences: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                         Length 2483
                                                                                                                                                                   Indels
                                                                                                                                                            396;
                                                                                                                                        Score 51.4; DB 3;
Pred. No. 0.013;
; Mismatches 396
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-08-946-617-1
                                                                                                                                        Match 5.0%;
Local Similarity 45.5%;
les 338; Conservative
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                                                                                                                                           Query Match
                                                                                                                                                       Best Loc
Matches
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                                                             CAAGGGATAATTCATCGTGATATAAAACCCAGTAATATTTTCTTTGCCCGGGATGATATA
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                                                                                                                                                TAACAAAATAGCAATATAAGTAATATTATACTACCACATTCTATAGAATTTTTAAATTG
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US-08-107-755A-8
Sequence 8, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Ento NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883
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APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTTATCAAATATAATTGAATATGAAT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
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                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEtentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELEPHONE: 904-372-5800
INFORMATION FOR SEQ 1D NO: 8;
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 1;
Pred. No. 0.036;
0; Mismatches 42
                                 A-1
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                                Suite
  NDENCE ADDRESS:
SEE: David R. Saliwanchik
: 2421 N.W. 41st Street, Gainesville
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Best Local Similarity 43.4%;
Matches 325; Conservative
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MOLECULE TYPE: 1
ORIGINAL SOURCE:
CORRESPONDENCE A
ADDRESSEE: Da
STREET: 2421
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LOCATION:
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LOCATION:
S-07-991-8678-8
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APPLICANT: MOYER, RICHARD W.
APPLICANT: MOYER, RICHARD W.
APPLICANT: Gruid!, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expl
NUMBER OF SEQUENCES: 77
CORRESPONDER ADDRESS:
ADDRESSE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville Gerard H. Bencen
STREET: FL
STATE: FL
STAT
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                                                                           AAATTTATCAAATATAATTGAATATGAAT
                                                                                                                                                                       US-08-544-332-8

Sequence 8, Application US/08544332

Patent No. 5935777

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Hall, Richard L.

APPLICANT: Gruidl, Michael E.
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MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 2;
Pred. No. 0.036;
0; Mismatches 4;
                                                                                                                                                                                                                      entemopoxvirus
                                                                                                                                                                                                                                                                                                                                      (234..782)
                                                                                                                                                                                                                                                                           . 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                      Amsacta moorei
                                                                                                                                                                                                                                                                              complement (18
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Best Local Similarity 43.4%;
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                   complement
                                                                                                                                                                                                                                                                                                                                                                            CDS
852..1511
                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
5-08-107-755A-8
                                                                                                                                                                                                                                                                         LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                        FEATURE
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Pred. No. 0.05;
0; Mismatches 222,
                                                                                                                          Version
 Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amsacta moorei entomopoxvirus
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELEPHONE: 904-375-8100
TELEFAX: 904-375-800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
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 41st Street,
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Best Local Similarity 47.7%;
Matches 207; Conservative
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STREET: 2421 N.W. CITY: Gainesville STATE: FL COUNTRY: USA ZIP: 32606
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3080.
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2502.
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MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: AMSA
FEATURE:
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FEATURE:
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                                                                                                                                       CAATTATTAATTCTATCGACATTTTTTTTTATTTGATATATTTTTTCAAAAAAA
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                                                     Length 1511
                                                                                  Indels
                                                                                420;
                                                      Score 49; DB 4;
Pred. No. 0.036;
); Mismatches 4
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APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: NO. 5476781el EI
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
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                                                      Query Match
Best Local Similarity 43.4%;
Matches 325; Conservative
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Sequence 1, Application U
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Rich
APPLICANT: Hall, Rich
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
 852..1511
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US-08-544-332-8
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RESULT 10
US-07-991-867B-25/c
; Sequence 25, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
                                                                                                                   774
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              437
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                                                                    ATGAGTTTTATTGGTGATTTATTGGCT---AGTAGTTATAGAGGTGCATTATTTATTCT
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COUNTRY: USA
ZIPE: 32606
COMPUTER: 126A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACECATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 19-FEB-1991
ATPORMATION NUMBER: US 07/657,584
FELEPHONE: 904-375-8100
TELEFAX: 904-372-8800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (genomic)
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LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                               908
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US-08-107-755A-1/C
Sequence 1, Application US/08107755A
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSE:
ADDRESSE:
ADDRESSE:
DAVID R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Cainesville
STREET: 32606
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
NRIOR DATE:
NRIOR APPLICATION DATA:
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                                                                      Length 1395
                                                                                                                             Indels
                                                                         Score 48.8; DB 1;
Pred. No. 0.039;
0; Mismatches 222;
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APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                        Query Match
Best Local Similarity 47.7%;
Matches 207; Conservative
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US-07-991-867B-25
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Query Match
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Pred. No. 0.048;
); Mismatches 222;
                                                                                                                                    Amsacta moorei entomopoxvirus
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORGANISM: Amsacta moorei entomopoxvi
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
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Best Local Similarity 47.78;
Matches 207; Conservative
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LOCATION:
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LOCATION:
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TOCATION:
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S-08-107-755A-1
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RESULT 12
US-08-107-755A-25/C
Sequence 25. Application US/08107755A
Sequence 15. Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: MOYET, RICHARD W.
APPLICANT: GAING, MICHAEL E.
TITLE OF INVENTION: No. 5721352el Entomopoxvi)
NUMBER OF EGUENCES: 40
CORRESPONDENCE: ADDRESS: 40
CORRESPONDENCE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galnesville
STRIET: Plorida
COUNTY: US.A.
STATE: Plorida
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
OPERATIOS STREM: PC-DS/MS-DS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/107,755A
FILING DATE: 19-760-1993
CLASSIFICATION NUMBER: US 07/627,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIN WINDER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOC
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Pred. No. 0.039;
0; Mismatches 222;
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NAME/KEY:
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US-08-544-332-1/C
; Sequence 1, Application US/08544332
; Patent No. 5935777
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard M.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
; UNBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gerard H. Bencen
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
                           196
                                                      894
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  834
                 ATATITGAAAATTICGGTACACCCAATTTAACTGATTITGAAGATGAATTATTTGTGAT
                                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                          STATE: FL
COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Vers
COMPUTER: PAtentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF 114.C4
TELECOMMUNICATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF 114.C4
TELECOMMUNICATION NUMBER: 35,746
REFERENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPER: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (65..1459)
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                                                                                                             GATTGGGATATTAT 908
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TOPOLOGY: unknown MOLECULE TYPE: DIORIGINAL SOURCE:
ORGANISM: Amsac
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NAME/KEY:
LOCATION
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                                                                                                                                                                                                                    Score 48.8; DB 4;
Pred. No. 0.05;
); Mismatches 222
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APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: NO. 5935777el En
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Sui
CITY: Gainesville
STATE: FL
COUNTRY: USA
z1F: 32606
COMPUTER READABLE FORM:
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complement (6277..6768)
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5-08-544-332-25/c
Sequence 25, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
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Best Local Similarity 47.7%;
Matches 207; Conservative
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STREET: 220 MONTOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUPUTER: CALIFORNIA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CULASSIFICATION NUMBER: US 08/422,711
FILING DATE: 10-CAT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: CO-CCT-1994
APPLICATION NUMBER: US 07/985,321
FRIDK APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FRIDK APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 10-CDEC-1992
ATTING DATE: 10-CDEC-1992
FILING DATE: 10-CDEC-1992
ATTING DATE: VA-DEC-1992
FILING DATE: VA-DEC-1992
FILING DATE: VA-DEC-1992
ATTING DATE: VA-DEC-1992
FILING DATE: VA-DEC-1993
ATTING DATE: VA-DEC-19
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NO.
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Sequence 9, Application US/08480604A

Patent No. 5736139

GENERAL INFORMATION:

APPLICANT: KINK, JOHN A.

APPLICANT: THALLEY, BRUCE S.

APPLICANT: PADHYE, NISHA V.

APPLICANT: FIRCA, JOSEPH R.

APPLICANT: STAFFORD, DOUGLAS C.

TITLE OF INVENTION: VACCINE AND ANT

TITLE OF INVENTION: PREVENTION OF C

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SC

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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Pred. No. 0.039;
); Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bencen, Gerard H.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: UF114.C4

TELECOMMUNICATION INFORMATION:

TELEFAX: 904-375-8100

TELEFAX: 904-375-800

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1395 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/5//
                                                                                                                                            US/08/544,332
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